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 Sent: Tuesday, March 04, 2003 4:00 PM
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 Subject: 10/017145 - sequence search request

10/017145 - sequence search request

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SEQ ID NO : 1

Thank you,

*Tekchand Saidha
 Primary Examiner
 Art Unit 1652, CMMI, Room No. 10D05
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 (703) 305-6595*

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 Patent Family: _____
 Other: _____

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Result No.	Score	Query Match	Length	DB ID	Description
1	1771	92.4	396	10 Q43140	043140 sesamum indicum
2	1757	91.7	396	10 Q43141	043141 sesamum indicum
3	1746	91.1	396	10 Q93X20	093X20 sesamum indicum
4	1733	90.4	401	10 O22832	022832 arabidopsis
5	1729	90.2	401	10 Q94AE9	Q94AE9 arabidopsis
6	1727	90.1	396	10 O24497	O24497 helianthus annuus
7	1701	88.8	396	10 O24498	O24498 helianthus annuus
8	1698	88.6	396	10 Q9SEK6	Q9SEK6 persica americana
9	1698	88.6	401	10 Q93X55	Q93X55 brassica napus
10	1676.5	88.5	409	10 Q9SWB7	Q9SWB7 arachis hypogaea
11	1695	88.5	401	8 Q9XQR7	Q9XQR7 brachypodium distachyon
12	1688	88.1	396	10 O65040	O65040 macadamia integrifolia
13	1673	87.3	396	10 Q8VXJ7	Q8VXJ7 helianthus annuus
14	1670	87.2	396	10 Q8VXJ8	Q8VXJ8 helianthus annuus
15	1660.5	86.7	407	10 Q42591	Q42591 arabidopsis thaliana
16	1653.5	86.3	396	10 Q8S059	Q8S059 oryza sativa

CC	-	-	SUBUNIT: HOMODIMER (BY SIMILARITY).
DR	-	-	SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
KW	-	-	SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
KW	Chloroplast; Fatty acid biosynthesis;		
TRANSIT peptide.	33		Oxidoreductase;
FT	TRANSPORTER_ACYL CARRIER PROTEIN DESATURASE.		
SEQUENCE	396 AA;	45168 MW;	A2345ABA676A0940 CRC64;
Query Match	92.4%	Score: 1771; DB 10;	Length: 396;
Best Local Similarity	91.28;	Pred. No. 7	6e-13;
Matches	331; Conservative	20;	Mismatches 12; Indels 0; Gaps 0;
QY	1	ASPLKSGSKVEVNKKPFMPPREVHVOYTHSMPPQKIEFKSLDNWAENILVHLKPEVK 60	Query Match 91.7%; Score: 1757; DB 10; Length: 396;
Ddb	34	ASPLRSGSKVEVNKKPFMPPREVHVOYTHSMPPQKIEFKSLDNWAENILVHLKPEVK 93	Best Local Similarity 90.6%; Pred. No. 1.e-135; Matches 349; Conservative 20; Mismatches 14; Indels 0; Gaps 0;
QY	61	CWQPQDFLDPDASGFDQVRERAKEIPIPDYFVVLGDMITEALPTYOTMLNTLDG 120	ASPLKSGSKVEVNKKPFMPPREVHVOYTHSMPPQKIEFKSLDNWAENILVHLKPEVK 60
Ddb	94	CWQPQDFLDPDASGFDQVRERAKEIPIPDYFVVLGDMITEALPTYOTMLNTLDG 153	ASPLRSGSKVEVNKKPFMPPREVHVOYTHSMPPQKIEFKSLDNWAENILVHLKPEVK 93
QY	121	VRDGETGASPTSWAIWTRAWTAEENRHGDLNNKYLYLSGRVDMRRIKETIQLTGSMDPR 180	ASPLKSGSKVEVNKKPFMPPREVHVOYTHSMPPQKIEFKSLDNWAENILVHLKPEVK 60
Ddb	214	VRDGETGASPTSWAIWTRAWTAEENRHGDLNNKYLYLSGRVDMRRIKETIQLTGSMDPR 213	ASPLRSGSKVEVNKKPFMPPREVHVOYTHSMPPQKIEFKSLDNWAENILVHLKPEVK 93
QY	154	VRDGETGASPTSWAIWTRAWTAEENRHGDLNNKYLYLSGRVDMRRIKETIQLTGSMDPR 213	ASPLKSGSKVEVNKKPFMPPREVHVOYTHSMPPQKIEFKSLDNWAENILVHLKPEVK 60
Ddb	181	TENSPYLGFLYTSEQRERATEFISHGNTAROAKEHGDKLAQICGTIAADEKRHETAYTKIV 240	ASPLRSGSKVEVNKKPFMPPREVHVOYTHSMPPQKIEFKSLDNWAENILVHLKPEVK 93
QY	214	TENSPYLGFLYTSEQRERATEFISHGNTAROAKEHGDNLKLAQICGTIAADEKRHETAYTKIV 273	ASPLKSGSKVEVNKKPFMPPREVHVOYTHSMPPQKIEFKSLDNWAENILVHLKPEVK 60
Ddb	241	EKFELIDPDTGTVLAFADMRKKISMPAHMLYDGRDDNLFDHESSAVAQLGVYTTAKDYADI 300	ASPLRSGSKVEVNKKPFMPPREVHVOYTHSMPPQKIEFKSLDNWAENILVHLKPEVK 93
QY	274	EKFELIDPDTGTVLAFADMRKKISMPAHMLYDGRDDNLFDHESSAVAQLGVYTTAKDYADI 333	ASPLKSGSKVEVNKKPFMPPREVHVOYTHSMPPQKIEFKSLDNWAENILVHLKPEVK 60
Ddb	301	LEFLVGGRKVYDKLTLGSAEFGQKAQDYCVGRLLPRIRRLEERAQGRAKEAPTMPFWIDFRQ 360	ASPLRSGSKVEVNKKPFMPPREVHVOYTHSMPPQKIEFKSLDNWAENILVHLKPEVK 93
QY	334	LEHVAVRKVANLTGLSADRGRKAQDYCVGLPPIRRLERAQGRAKQPKIFFSWIDRE 393	ASPLKSGSKVEVNKKPFMPPREVHVOYTHSMPPQKIEFKSLDNWAENILVHLKPEVK 60
Ddb	361	VKL 363	ASPLRSGSKVEVNKKPFMPPREVHVOYTHSMPPQKIEFKSLDNWAENILVHLKPEVK 93
QY	394	VQL 396	ASPLKSGSKVEVNKKPFMPPREVHVOYTHSMPPQKIEFKSLDNWAENILVHLKPEVK 60
RESULT 2			
Q43141	Q43141	PRELIMINARY;	PRT; 396 AA.
ID	Q43141;		RESULT 3
DT	01-NOV-1996 (TREMBLrel. 01, Created)	ID	093320 PRELIMINARY; PRT; 396 AA.
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)	AC	093320; PRELIMINARY; PRT; 396 AA.
DE	Acyl-[acyl]-carrier protein desaturase (EC 1.14.99.6) (Stearoyl-ACP desaturase).	DT	01-DEC-2001 (TREMBLrel. 19, Created)
OS	Sesamum indicum (Oriental sesame) (Gingelly).	DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicots; core eudicots; Asteridae; euasterids I; Lamiales; Pedaliaceae; Sesamum. [1]	OC	01-JUN-2002 (TREMBLrel. 21, Last annotation update)	
NCBI_TaxID=4182; OX	OC	DE Destroy acyl carrier protein.	
SEQUENCE FROM N.A.	OC	OS Sesamum indicum (Oriental sesame) (Gingelly).	
SEQUENCE FROM N.A.	OC	OC Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; core eudicots; OC Asteridae; euasterids I; Lamiales; Pedaliaceae; Sesamum.	
RP	NCBI_TaxID=4182;	RC SEQUENCE FROM N.A.	
RN		RC TISSUE=DEVELOPING SEED;	
RP		RC Chopra V.L.;	
RT		RA RA "transgenic expression of cDNA encoding stearoyl acyl carrier protein desaturase of sesamum indicum in Indian mustard."	
CC		RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.	
CC		RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.	
CC		RN [2] SEQUENCE FROM N.A.	
CC		RP SEQUENCE FROM N.A.	
CC		RC TISSUE=DEVELOPING SEED;	
CC		RC Chopra V.L.;	
CC		RA RA "transgenic expression of cDNA encoding stearoyl acyl carrier protein desaturase of sesamum indicum in Indian mustard."	
CC		RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.	
CC		RN [3] SEQUENCE FROM N.A.	
CC		RP	

RN	TISSUE=DEVELOPING SEED;	
RA	Chopra V.L.	
RT	"Transgenic Indian mustard high in oleate.";	
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.	
DR	EMBL: AJ31331; CAC4732.1;	
DR	InterPro: IPR00367; FA_desaturase.	
DR	InterPro: IPR001225; FA_desaturase.	
DR	Pfam: PF03405; FA_desaturase_2; 1.	
DR	PROSITE: PS00574; FATTY_ACID_DESATURASE_2; UNKNOWN_1.	
SQ	SEQUENCE 396 AA; 45054 MW; 454DFAC6687BEB2 CRC64;	
Query Match	91.1%; SCORE 1746; DB 10; Length 396;	
Best Local Similarity	89.8%; Pred. No. 8.5e-135; Gaps 0;	
Matches	326; Conservative 21; Mismatches 16; Indels 0; Gaps 0;	
QY	1 ASTLRSKSGMEVNIKKPMPMPREVHQVTHSMPPQKIEFKSLDNWAEENILVLHKPVK 60	
Db	34 CWPQDFLPLPDAASDGFDECVRERAKEIIPDDFVVVLGDMITEALPTYQTMNLNTLDG 93	
QY	61 CWPQDFLPLPDAASDGFDECVRERAKEIIPDDFVVVLGDMITEALPTYQTMNLNTLDG 120	
Db	94 CWPQDFLPLPSSGDFDQVKERAKEIIPDDFVVVLGDMITEALPTYQTMNLNTLDG 153	
QY	121 VDDETGSAPTSWAIWTRWTAEEHRHGDLLNKYLQLLSGRVMDPPIEKTQYLGSGMDP 180	
Db	154 VRENTGASPTSWAIWTRWTAEEHRHGDLLNKYLQLLSGRVMDP 213	
QY	181 TENSPLYGLIYTTSQERTATFISHTGNTRQAKEHEDIKLIAQICGTTAIDEKRHETAYTKIV 240	
Db	214 EKLFEIDNDTVAFADEMRKIKTSPMAHLMYDGRDDNLFDHFSAAQRLGVYTAKDYADI 273	
QY	241 EKLFEIDNDTVAFADEMRKIKTSPMAHLMYDGRDDNLFDHFSAAQRLGVYTAKDYADI 300	
Db	274 EKLFEIDNDTVAFADEMRKIKTSPMAHLMYDGRDDNLFDHFSAAQRLGVYTAKDYADI 333	
QY	301 LELFLVGKVKDQKLTLGSAEQKAQDYVCBLPPRTRLEERQGRAKEAPTMPESWIFDRO 360	
Db	334 LEHLVAROKVANLTGLSADCQRAQDYVCCLPPRTRLEERQGRAKOAPKPSKVHDRE 393	
QY	361 VKL 363	
Db	394 VQL 396	
RESULT 4		
ID O22832	PRELIMINARY; PRT; 401 AA.	
AC O22832;		
DT 01-JAN-1998	(TREMBLrel. 05, Created)	
DT 01-JUN-1998	(TREMBLrel. 05, Last sequence update)	
DT 01-JUN-2002	(TREMBLrel. 21, Last annotation update)	
DE	Acyl-(acyl-carrier protein] desaturase (EC 1.14.99.6) (Stearoyl-ACP desaturase).	
DE	ATPG43710 OR SS12.	
OS	Arabidopsis thaliana (Mouse-ear cress).	
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.	
OX	NCBI_TaxID=3702;	
RN	SEQUENCE FROM N.A.	
RC	STRAIN=CV ; COLUMBIAN;	
RD	LINE=20083487; PubMed=10617197;	
RA	Lin X., Kaul S., Rounstley S.D., Shea T.P., Benito M.-I., Town C.D., Buell C.R., Ketchum K.A., Lee J.J., Roening C.M., Koo H., Moffat K.S., Cronin C.Y., Mason T.M., Bowm C.L., Barnstead L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Salzberg S.L., Fraser C.M., Venten J.C., White O., Eisen J.A.,	
RA	"Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.", Nature 402:761-768(1999).	
RT		
RL		
[2]	SEQUENCE FROM N.A.	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=CV . COLUMBIA;	
RA	Lin X.;	
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.	
RN	SEQUENCE FROM N.A.	
RP	SEQUENCE FROM N.A.	
CC	MEDLINE=21314454; PubMed=11481500;	
CC	RX	
RA	Kachroo P., Shanklin J., Shah J., Whittle E.J., Klessig D.F.; "A fatty acid desaturase modulates the activation of defense signaling pathways in plants."	
RT	"A fatty acid desaturase modulates the activation of defense signaling pathways in plants."	
RT	Pathways in plants;"	
RL	Proc. Natl. Acad. Sci. U.S.A. 98:9448-9453(2001).	
CC	-1 - FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL CHAIN (BY SIMILARITY).	
CC	-1 - CATALYTIC ACTIVITY: STEAROYL-[ACYL-CARRIER PROTEIN] + AH(2) + O(2) = OLEOYL-[ACYL-CARRIER PROTEIN] + A + 2 H(2)O.	
CC	-1 - CARRIER: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH (BY SIMILARITY).	
CC	-1 - PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE OILS.	
CC	-1 - SUBUNIT: HOMODIMER (BY SIMILARITY).	
CC	-1 - SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).	
CC	-1 - SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.	
DR	InterPro: IPR005067; FA_desat.	
DR	InterPro: IPR012345; FA_desat.	
DR	InterPro: IPR01405; FA_desat.	
DR	EMBL: AC002313; AAB64035; 1.	
DR	EMBL: AF395441; AAK85232; 1.	
DR	HSSP: P22337; 1AFR.	
DR	InterPro: IPR005067; FA_desat.	
DR	InterPro: IPR012345; FA_desat.	
DR	InterPro: IPR01405; FA_desat.	
DR	PROSITE: PS00574; FATTY_ACID_DESATUR_2; 1.	
KW	Chloroplast; Fatty acid biosynthesis; NADP; Oxidoreductase; KW	
KW	Chloroplast; Fatty acid biosynthesis; NADP; Oxidoreductase; KW	
SEQUENCE 401 AA:	455693 MW: 0C46984578D4E1D1 CRC64;	
Query Match	90.4%; Score 1733; DB 10; Length 401;	
Best Local Similarity	89.4%; Pred. No. 1e-133; Matches 22; Mismatches 16; Indels 0; Gaps	
Matches	322; Conservative 22; Mismatches 16; Indels 0; Gaps	
QY	4 LKSGSKVEYNLKKPFMPPREVHCVYQTMNLNTLDGVKD 63	
Db	42 LSSGPKEYEVESLKKPFTPPREVHCVLHSAPPQKIEFKSMEVNWBANLLHLKDVKEWSQ 101	
QY	64 PQDFLPDPASDGFDEQVRLERAKEIPDDFYVVLGDMITEALPTYQTMNLNTLDGVRD 123	
Db	102 PQDFLPDPASDGFDEQVRLERARELPDDFYVVLGDMITEALPTYQTMNLNTLDGVRD 161	
QY	124 ETGASPTSWAIWTRWTAEEHRHGDLLNKYLQLLSGRVMDPRTEN 183	
Db	162 ETGASPTSWAIWTRWTAEEHRHGDLLNKYLQLLSGRVMDPRTEN 221	
QY	184 SPYLGFYTTSQERATFISHGNTAQRQKADKHEGDIKLAQICGTIAADEKRHETAYTKIV 243	
Db	222 NPFLGFTTSQERATFISHGNTAQRQKADKHEGDIKLAQICGTIAADEKRHETAYTKIV 281	
QY	244 FEIDPDGTIVAFADMRRKKISMPPAHLYDGRDDNLFDHESAVAQRLGVYTAKDYADILEF 303	
Db	282 FEIDPDGTIVAFADMRRKKISMPPAHLYDGRDDNLFDNFSSVAQRLGVYTAKDYADILEF 341	
RESULT 5		
ID Q94AE9	PRELIMINARY; PRT; 401 AA.	
AC Q94AE9;		
DT 01-DEC-2001	(TREMBLrel. 19, Created)	
DT 01-DEC-2001	(TREMBLrel. 19, Last sequence update)	
DT 01-JUN-2002	(TREMBLrel. 21, Last annotation update)	
DE A22943710/F18019-18.		

AC	Q24498;	RESULT: 8
DT	01-JAN-1998 (TREMBLrel. 05, Created)	09SEK6
DR	01-JAN-1998 (TREMBLrel. 05, Last sequence update)	PRELIMINARY;
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)	FRT;
DB	Acy-l-acyl-carrier protein] desaturase (EC 1.14.99.6) (Stearoyl-ACP desaturase).	396 AA.
DE	Helianthus annuus (Common sunflower).	
OS	Spermatophytidae; Streptophytidae; Embryophytidae; Tracheophytidae; Viridiplantae; Magnoliophytidae; eu dicots; core eu dicots; Asteridae; euasterids II; Asterales; Asteraceae; Asteroidae; Heliantheae; Helianthus.	
OC		
OC		
OX		
NCBI_TaxID	4232;	
RN	[1]	
RP	SEQUENCE FROM N_A.	
RC	STRAIN=MAMMOTH;	
RA	Hongtrakul V., Slabough M.B., Knapp S.J.;	
RA	Sunflower stearoyl-ACP desaturase;	
RL	Submitted (FEB-1997) to the ENBL/GenBank/DDBJ databases.	
CC	-!- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A CTS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL CHAIN (BY SIMILARITY).	
CC	-!- CATALYTIC ACTIVITY: STEAROYL-[ACYL-CARRIER PROTEIN] + AH(2) + O(2) = OLEOYL-[ACYL-CARRIER PROTEIN] + A + 2 H(2)O.	
CC	-!- COFACTOR: FERREDOXIN FERREDOXIN NADPH REDUCTASE, AND NADPH (BY SIMILARITY).	
CC	-!- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE OILS.	
CC	-!- SUBUNIT: HOMODIMER (BY SIMILARITY).	
CC	-!- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).	
CC	-!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.	
DR	EMBL: U91340; AAB6145.1; -.	
DR	HSSP: P22337; IAFR.	
DR	InterPro: IPR05067; FA_desat.	
DR	DR: IPR01225; FA_desaturase.	
DR	Pfam: PF03405; FA_desaturnase_2; 1.	
DR	PROSITE: PS00574; Fatty_ACID_DESATUR_2; 1.	
KW	Chloroplast; Fatty acid biosynthesis; NADP; Oxidoreductase; Transit peptide.	
SQ	SEQUENCE 396 AA: 45112 MW: C9DB8CD04310BFA CRC64;	0;
Query Match	88.0%; Score 1701; DB 10; Length 396;	
Best Local Similarity	88.4%; Pred. No. 4 2e-131;	
Matches	321; Conservative 18; MisMatches 24; Indels 0; Gaps 0;	
Qy	1 ASTLIGSGKEVENLKKPFMPREVIQVTHSMPPKTIETKSLDWAENILVHLKPVEK 60	
Db	34 ASTIGGATKVESTKRKPFTPREVHQVLSMPPKTIETKSMEWAEDILVHLKPVEK 93	
Qy	61 CWQPQDFLPDASDGFDQEYRELREKAFPDDYFVVLGDMITEALPYQTMLNTLG 120	
Db	94 CWAQDFLPDASDGFMEQVEELRAREKAFPDDYFVVLGDMITEALPYQTMLNTLG 153	
Qy	121 VRDETGAСПSWAIWTRAWTAENRGLINKLYLGSGRDMQREKTIQYLIGSGMDPR 180	
Db	154 VRDETCAСПSWAIWTRAWTAENRGLINKLYLGSGRDMQREKTIQYLIGSGMDPR 213	
Qy	181 TENSPYLGFIYTSFQRATFISHGNTARQKEHGDYKLAQCGTIAADEERHETAYTKIV 240	
Db	214 TENSPYLGFIYTSFQRATFISHGNTARHAKREHGDYKLAQCGTIAADEERHETAYTKIV 273	
Qy	241 EKLFEILDPGTVLAFADMRRKISMPAHLMYGRDDNLFLFNSAVAQRLGVYTARDYADI 300	
Db	274 EKLFEILDPGTVLAFADMRRKISMPAHLMYGRDDNLFLFNSAVAQRLGVYTARDYADI 333	
Qy	301 LEFLYGRWKVDKLTLGSLAEGQKAQDYVCRLPRIRLEERAQGRAKEAPIMPSWLFDRQ 360	
Db	334 LEFLYGRWKVADLTGSLGEGRKAQDVCGLAPRIRLEERSARAKESVNPSWLFDR 393	
Qy	361 VKL 363	
Db	394 VKL 396	
Query Match	88.6%; Score 1698; DB 10; Length 396;	
Best Local Similarity	87.1%; Pred. No. 7 3e-131;	
Matches	316; Conservative 27; MisMatches 20; Indels 0; Gaps 0;	
Qy	1 ASTLIGSGKEVENLKKPFMPREVIQVTHSMPPKTIETKSLDWAENILVHLKPVEK 60	
Db	34 ASTLRSSTKEYDNIKKPFSPPREVHTQVTHSMPPKTIETKSLDWAENILVHLKPVEK 93	
Qy	61 CWQPQDFLPDASDGFDQEYRELREKAFPDDYFVVLGDMITEALPYQTMLNTLG 120	
Db	94 CWQPQDFLPDASDGFMEQVEELRAREKAFPDDYFVVLGDMITEALPYQTMLNTLG 153	
Qy	121 VRDETGAСПSWAIWTRAWTAENRGLINKLYLGSGRDMQREKTIQYLIGSGMDPR 180	
Db	154 VRDETCAСПSWAIWTRAWTAENRGLINKLYLGSGRDMQREKTIQYLIGSGMDPR 213	
Qy	181 TENSPYLGFIYTSFQRATFISHGNTARQKEHGDYKLAQCGTIAADEERHETAYTKIV 240	
Db	214 TENSPYLGFIYTSFQRATFISHGNTARHAKREHGDYKLAQCGTIAADEERHETAYTKIV 273	
Qy	241 EKLFEILDPGTVLAFADMRRKISMPAHLMYGRDDNLFLFNSAVAQRLGVYTARDYADI 300	
Db	274 EKLFEILDPGTVLAFADMRRKISMPAHLMYGRDDNLFLFNSAVAQRLGVYTARDYADI 333	
Qy	301 LEFLYGRWKVDKLTLGSLAEGQKAQDYVCRLPRIRLEERAQGRAKEAPIMPSWLFDRQ 360	
Db	334 LEFLYGRWKVADLTGSLGEGRKAQDVCGLAPRIRLEERSARAKESVNPSWLFDR 393	

AC Q42591;
DT DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Acyl-[acyl-carrier protein] desaturase (EC 1.14.99.6) (Stearoyl-ACP
desaturase).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TAXID:3702;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-AERIAL PARTS;
RA Piffanelli P.; Murphy D.J.;
RT "Cloning of a stearoyl-ACP desaturase from Arabidopsis thaliana."
RL Submitted (Nov-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A
CC CTS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
CC CHAIN (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: STEAROYL-[ACYL-CARRIER PROTEIN] + AH(2) + O(2)
CC = OLEOYL-[ACYL-CARRIER PROTEIN] + A + H(2)O
CC -!- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH (BY
CC SIMILARITY).
CC -!- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
CC ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
CC OILS.
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
DR EMBL: X93461; CAA63746.1;
DR HSSP: P3337; IAFR.
DR InterPro: IPR005067; FA_desat.
DR InterPro: IPR01225; FA_desaturase.
DR PFAM: PF03405; FA_desaturase_2;
DR PROSITE: PS00574; FATTY_ACID_DESATURASE_2;
KW Chloroplast; Fatty acid biosynthesis; NADP; Oxidoreductase;
KW transpeptidase.
SQ Sequence 407 AA: 46102 MW: 82351490844296 CRC64;

Query Match 86.7%; Score 1660.5; DB 10; Length 407;
Best Local Similarity 87.9%; Pred. No. 9e-128;
Matches 311; Conservative 21; Mismatches 17; Indels 5; Gaps 1;

4 LKSGSKREVENKKPFMPPREYHVQVTHSMPPQQKIEFLFKSLDNWAEEENLHLKPVEKCWQ 63
Db 42 LSSGPREVESSLKKPFPPEYHVQVLSMPPQKIEFLFKSLDNWAEEENLHLKPVEKSQ 101
Qy 64 PQDFLPPDPSDGFDEQYRELRERAKETPDYFVVLGDMITEALAPTYQTMNLTDGVRD 123
Db 102 PQDFLPPDPSDGFEDQYRELRERAKETPDYFVVLGDMITEALAPTYQTMNLTDGVRD 161
Qy 124 ETGASPTSWA1WTRATAENRHDGLLNKYLYLSGRVDMROQEKTIQYLGSGMQPRTE 183
Db 162 ETGASPTSWA1WTRATAENAHGDGLLNKYLYLSGRVDMROQEKTIQYLGSGMQPRTE 221
Qy 184 SPYLGFITYTTSQERATFISHGNTARQAEHKCDIKLAQICGTIAADEKRHETAYTKEKL 243
Db 222 NPYLGFITYTTSQERATFISGNTARQAEHKCDIKLAQICGTIAADEKRHETAYTKEKL 281
Qy 244 FEIDPDGTVALFADMRRKKISMPAHLYMDGRDNLFDFHESAVAQRUGVYTAKDYADILEP 303
Db 282 FEIDPDGTVALFADMRRKKISMPAHLYMDGANDNLFDFNSSSAQRUGVYTAKDYADILEP 341
Qy 304 LVGRWKVDKTLGLSAGQKAQDYVCRLPPTIRRRLBERAQGRAK-----EAPTMP 352
Db 342 LVGRWKQDGLTGSLSGEGNAQDYLCLGSLAPRKRLDERAQRALKGQRQPKLP 395

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Result No.	Score	Query	Match	Length	DB ID	Description
1	1916	100.0	396	1	STAD_RICCO	P22337 ricinus com
2	1764	92.1	396	1	STAD_CUCSA	P32061 cucumis sat
3	1752	'91.4	396	1	STAD_CARTI	P22243 carthamus t
4	1738	90.7	411	1	STAD_SOYBN	Q42807 glycine max
5	1724.5	90.0	399	1	STAD_SFOL	P28645 spinacia ol
6	1698	88.6	398	1	STAD_BRANA	P29108 brassica na
7	1680	87.7	399	1	STAS_BRANA	Q24428 brassica na
8	1662.5	86.8	393	1	STAD_ELAGV	Q24428 brassica na
9	1655	86.4	396	1	STAD_HELAN	Q96456 helianthus
10	1652	86.2	393	1	STAD_SOLOCO	Q91319 solanum com
11	1649	86.1	390	1	STAD_OBEU	Q43593 olea europ
12	1626	84.9	393	1	STAD_SOLTU	P46253 solanum tub
13	1610.5	84.1	397	1	STAD_GOSHI	Q42770 gossypium h
14	1607	83.9	398	1	STAD_SMICH	Q01753 simmondsia
15	1583	82.6	390	1	STAD_ORYSIA	Q40731 oryza sativ
16	1465	76.5	396	1	STAD_LINUS	P32062 linnus usita
17	1317	68.7	385	1	STAD_CORSIA	P57195 burchnera ap
18	104.5	5.5	665	1	TKT_BUGAI	P28955 equine herp
19	101.5	5.3	3421	1	TEGU_HSVEB	Q10178 schizosacch
20	101	5.3	1188	1	S3B1_SCHPO	P00453 escherichia
21	99.5	5.2	375	1	RIR2_ECOLI	O75533 homo sapien
22	98.5	5.1	1304	1	S3B1_HUMAN	Q99nb9 mus musculu
23	98.5	5.1	1304	1	S3B1_MOUSE	O57683 xenopus lae
24	98.5	5.1	1307	1	S3B1_XENFLA	O60071 schizosacch
25	97.5	5.1	449	1	YBB9_SCHPO	Q9z930 chlamydia p
26	97	5.1	820	1	SYL_CHPN	Q9vn5 drosophila
27	97	5.1	2096	1	BP28_DROME	P41121 photorhabdu
28	96.5	5.0	709	1	PNP_PHOLO	P43553 saccharomy
29	96	5.0	858	1	ALR2_FEAST	P37427 salmonella
30	95.5	5.0	375	1	RIR2_SALTY	Q59105 alcaligenes
31	93.5	4.9	643	1	NOSZ_ALCEU	Q60504 homo sapien
32	93.5	4.9	671	1	VINE_HUMAN	Q10202 schizosacch
33	92.5	4.8	578	1	YBX6_SCHPO	

ALIGNMENTS					
RESULT 1					
STAD_RICCO	STANDARD;				
ID STAD_RICCO					
AC P22337;					
DT 01-AUG-1991 (Rel. 19, Created)					
DT 01-AUG-1991 (Rel. 19, Last sequence update)					
DT 15-JUN-2002 (Rel. 41, Last annotation update)					
DE Acyl-acyl-carrier protein desaturase, chloroplast precursor					
DE (EC 1.14.99.6) (Stearoyl-ACP desaturase) (Delta(9) stearoyl-acyl carrier protein desaturase).					
OS Ricinus communis (Castor bean), Viridiplantae; Streptophytina; Embryophyta; Tracheophyta; Spermatophytina; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; euroids 1; Malpighiales; Euphorbiaceae; Ricinus [1]					
RN SEQUENCE FROM N.A. MEDLINE=91172837; PubMed=20061817;					
RX RA Shanklin J., Somerville C.R.;					
RT RT structurally unrelated to the animal and fungal homologs.";					
RL Proc. Natl. Acad. Sci. U.S.A. 88:2510-2514 (1991). [1]					
RN RN [2]					
RP RP SEQUENCE FROM N.A.					
RC TISSUE=Endosperm;					
RA Knutson D. S., Scherer D.E., Schreckengost W.E.;					
RT RT "Nucleotide sequence of a complementary DNA clone encoding stearoyl-acyl carrier protein desaturase from castor bean, Ricinus communis.";					
RT RT acyl carrier protein desaturase from castor bean, Ricinus communis.";					
RL Plant Physiol. 96:344-345(1991). [3]					
RN RN X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).					
RX RX MEDLINE=97015109; PubMed=8861937; Lindqvist V., Huang W., Schneider G., Shanklin J.; "Crystal structure of delta-9 stearoyl-acyl carrier protein desaturase from castor seed and its relationship to other di-iron proteins."; EMBO J. 15:4081-4092(1996).					
CC CC -!- FUNCTION: CONVERSES STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL CHAIN.					
CC CC -!- CATALYTIC ACTIVITY: Stearoyl-lacyl-carrier protein] + AH(2) + O(2) + H(2)O.					
CC CC = oleoyl-lacyl-carrier protein] + A + 2 H(2)O.					
CC CC -!- COFACTOR: FERRREDOXIN, FERRREDOXIN REDUCTASE, AND NADPH.					
CC CC -!- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE OILS.					
CC CC -!- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF NONPHOTOSYNTHETIC TISSUES.					
CC CC -!- TISSUE SPECIFICITY: HIGHER LEVELS IN DEVELOPING SEEDS THAN IN LEAF AND ROOT TISSUES.					
CC CC -!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.					

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CC [2] SEQUENCE FROM N.A.; Pubmed=2006187;
 CC MEDLINE=91172837;

CC Shanklin J., Somerville C.;
 CC RT Stearoyl-acyl-carrier-protein desaturase from higher plants is
 CC structurally unrelated to the animal and fungal homologs.";
 DR EMBL: X59857; AAAT4692-1; ALT_INIT.
 DR PIR: S16463; OHCSAD.
 DR PIR: A39170; A39170.
 DR PDB: 1AFR; 15-MAY-97.
 DR InterPro; IPR00567; FA_desat.
 DR InterPro; IPR001225; FA_desatursate_2; 1.
 DR PFAM; PF03405; FA_desatursate_2; 1.
 DR PROSITE; PS00574; FATTY_ACID_DESATUR_2; 1.
 DR Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;
 KW Transit peptide; 3D-structure.
 FT TRANSIT 1 33 CHLOROPLAST (BY SIMILARITY).
 FT CHAIN 34 396 MW: E50DA725936392AF CRC64;
 SQ SEQUENCE 396 AA; 45371 MW: E50DA725936392AF CRC64;

Query Match Score 1916; DB 1; Length 396;
 Best Local Similarity 100.0%; Pred. No. 2e-140;
 Matches 363; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 ASTLKGSKKEVNLLKKPMPPEVHYQVTHSMPPQKIEIFKSLDNWAENILVHLKPVEK 60
 Db 34 ASTLKGSKKEVNLLKKPMPPEVHYQVTHSMPPQKIEIFKSLDNWAENILVHLKPVEK 93

Qy 61 CROPQDFLPDPASDGFDEQVRLRERAKEIPDPDYFVVLGMDITEPALPTYQTMINTLDG 120
 Db 94 CROPQDFLPDPASDGFDEQVRLRERAKEIPDPDYFVVLGMDITEPALPTYQTMINTLDG 153

Qy 121 VRIETGASPSTWAIWTRAWTAENRHGDLLNKYLGSRVDMRQIEKTIQYLGSGMOP 180
 Db 154 VRIETGASPSTWAIWTRAWTAENRHGDLLNKYLGSRVDMRQIENTIQYLGSGMOP 213

Qy 181 TENSPLYGFTTYSQERTFISHGNTARQAKHGDIKLAQTCIGTIAADEKRHETAVTKIV 240
 Db 214 TENSPLYGFTTYSQERTFISHGNTARQAKHGDIKLAQIGTIAADEKRHETAVTKIV 273

Qy 241 EKLFEIFDPGTVAFADEMRKIKISMPAHLMYGRDDNFIDHESAVAOQLGYTAKYADI 300
 Db 274 EKLFEIFDPGTVAFADEMRKIKISMPAHLMYGRDDNLFDHESAVAOQLGYTAKYADI 333

Qy 301 LEFLVGRMKVKDQKUTGLSAEGOKAQDYICRLPPRIRLERAEQGRAKBAPTMFSWIFDQ 360
 Db 334 LEFLVGRMKVKDQKUTGLSAEGOKAQDYICRLPPRIRLERAEQGRAKBAPTMFSWIFDQ 393

Qy 361 VKL 363
 Db 394 VKL 396

RESULT 2
 STAD_CUCSA STANDARD; PRT; 396 AA.
 AC P32061; STAD_CUCSA STANDARD;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-15-TUN-2002 (Rel. 41, Last annotation update)
 DE Acyl-(acyl-carrier protein) desaturase, chloroplast precursor
 OS Cucumis sativus (Cucumber).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; Rosidae;
 OC euroids I; Cucurbitales; Cucurbitaceae; Cucumis.
 NCBT_TaxID=3639;
 RN SEQUENCE FROM N.A.
 RC TISSUE=Seedling cotyledon;
 RA Shanklin J., Mullins C., Somerville C.R.;
 RT "Sequence of a complementary DNA from *Cucumis sativus* L. encoding the
 stearoyl acyl-carrier protein desaturase.";
 RL Plant Physiol. 97:467-468(1991).

Page 4

RT	"Modification of Brassica seed oil by antisense expression of a stearoyl-acyl carrier protein desaturase gene";	Db	343 WKIESLTGLSGEGGNKAQEYICGGLPFRRLDERAQARAKKGPKVFFSWIHDREVQL 398
RL	Proc. Natl. Acad. Sci. U.S.A. 89:2624-2628(1992).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
STRAIN=cv; JET nefuf; TISSUE=Leaf;		RESULT 7	
RX MEDLINE=97260965; PubMed=9107041;		ID STAS_BRANA STANDARD; PRT; 399 AA.	
RX MEDLINE=01-APR-1993 (Rel. 25, Created)		AC 001771;	
RX MEDLINE=01-APR-1993 (Rel. 25, Last sequence update)		DT 01-APR-1993	
RT "Intra- and extracellular lipid composition and associated gene expression patterns during pollen development in <i>Brassica napus</i> .";		DT 15-JUN-2002 (Rel. 41, Last annotation update)	
RT Plant J. 11:549-562(1997).		DE ACyl-acyl-carrier protein desaturase, seed specific, chloroplast precursor (EC 1.14.99.6) (Stearoyl-ACP desaturase).	
CC -!- FUNCTION: Converts Stearoyl-ACP to Oleoyl-ACP by introduction of a cis double bond between carbons delta-9 and delta-10 of the acyl chain.		DE precursor (EC 1.14.99.6) (Stearoyl-ACP desaturase).	
CC -!- CATALYTIC ACTIVITY: Stearoyl-acyl-carrier protein + AH(2) + O(2) = Oleoyl-acyl-carrier protein + A + 2 H(2)O.		OS <i>Brassica napus</i> (Rape).	
CC -!- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.		OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytina; Magnoliophyta; Eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.	
CC -!- PATHWAY: Catalyzes the principal conversion of saturated fatty acids to unsaturated fatty acids in the synthesis of vegetable oils.		OC NCBI_TAXID=3706;	
CC -!- SUBUNIT: Homodimer.		RN [1]	
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF NONPHOTOSYNTHETIC TISSUES.		RP SEQUENCE FROM N.A.	
CC -!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.		RC STRAIN=cv; Jet nefuf; TISSUE=Embryo;	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	RX MEDLINE=9338575; PubMed=1515603;	
CC	-----	RA Slocombe S.P., Cummins I., Jarvis R.P., Murphy D.J.; RT Nucleotide sequence and temporal regulation of a seed-specific desaturase.;	
CC	-----	RT Plant Mol. Biol. 20:151-155(1992).	
CC	-----	CC -!- FUNCTION: Converts Stearoyl-ACP to Oleoyl-ACP by introduction of a cis double bond between carbons delta-9 and delta-10 of the acyl chain.	
CC	-----	CC -!- CATALYTIC ACTIVITY: Stearoyl-acyl-carrier protein + AH(2) + O(2) = Oleoyl-acyl-carrier protein + A + 2 H(2)O.	
CC	-----	CC -!- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.	
CC	-----	CC -!- PATHWAY: Catalyzes the principal conversion of saturated fatty acids to unsaturated fatty acids in the synthesis of vegetable oils.	
CC	-----	CC -!- SUBUNIT: Homodimer (by similarity).	
CC	-----	CC -!- SUBCELLULAR LOCATION: Chloroplast (probable).	
CC	-----	CC -!- TISSUE SPECIFICITY: Developing seed.	
CC	-----	CC -!- DEVELOPMENTAL STAGE: Induced by 25 days after anthesis (DAA), peaking at 45 DAA but decreasing considerably thereafter.	
CC	-----	CC -!- SIMILARITY: Belongs to the fatty acid desaturase family.	
CC	-----	-----	
CC	-----	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	
CC	-----	CC	
DR	X60978; CAA43294_1; -.	CC	
DR	X97325; QAA65990_1; -.	CC	
DR	S23351; S23351.	CC	
DR	HSSP_P22337; 1AFR.	CC	
DR	InterPro; IPRO05067; FA_desat.	CC	
DR	InterPro; IPRO01225; FA_desaturase.	CC	
DR	Pfam; PF03405; FA_desaturase_2; 1.	CC	
DR	PROSTER; PS00544; Fatty_acid_desaturase_1.	CC	
KW	Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast; Transit peptide.	CC	
KW	Transit peptide.	CC	
FT	1 34 CHLOROPLAST (BY SIMILARITY).	CC	
FT	35 398 ACYL-(ACYL-CARRIER PROTEIN) DESATURASE.	CC	
FT	SEQUENCE 398 AA: 4534 MW: 906689FCFE41C5F5 CRC64;	CC	
FT	Query Match 88.6%; Score 1698; DB 1; Length 398; Best Local Similarity 88.2%; Pred. No. 1..3e-123; Matches 314; Conservative 27; N mismatches 27; Indels 0; Gaps 0;	DR	
FT	SEQUENCE 8 SKEVENLKEFMPPEVHVQVTHNMPPQKEIPLDNLWVHLPKPEVKWPQDF 67 43 SKEVESSLKEFMPPEVHVQVTHNMPPQKEIPLDNLWVHLPKPEVKWPQDF 102	DR	
FT	68 LPDPASDGFEQVRRLERAKEIPLDDYFVVLGDMITEALPLPTQTMNLNTLGVRDETGA 127 103 LPDPASDGFDQVRLLERARELPLDYFVVLGDMITEALPLPTQTMNLNTLGVRDETGA 162	DR	
FT	128 SPTSKAIWTRAWTAENRHDLANKLYLSGRVDMQRIENTQYLIGSMMDPRTENSPYL 187 163 SPTSKAIWTRAWTAENRHDLANKLYLSGRVDMQRIENTQYLIGSMMDPRTENNPYL 222	DR	
FT	188 GFIVTSFQERATFISHGNPQKAEHQVQVTHNMPPQKEIPLDNLWVHLPKPEVKWPQDF 247 223 GFIVTSFQERATFISHGNPQKAEHQVQVTHNMPPQKEIPLDNLWVHLPKPEVKWPQDF 282	DR	
FT	248 PDGTIVLAFAFMMRKTISMPAHLYMDGRDNLFHPSAVAGRLGTTAKDYLADILEFLYGR 307 283 PDGTIVMAFMMRKTISMPAHLYMDGRDEELFDNFSSVAGRLGTTAKDYLADILEFLYGR 342	DR	
FT	308 WKVDKLGTGSLSAEGOKAQDYVCRLLPPIRRLERAEQRAKEAPTMPSWIFDRQVKL 363 328 PKEVNEKKKPMPMPREHVQVTHNMPPQKEIPLDNLWVHLPKPEVKWPQDF 67 44 SKEVEISKKPPTPVPREVHLQVLSHMPQKIEFKMSMEDAQNLLHLDKVEKSMPQDF 103	DR	
FT	329 PKEVNEKKKPMPMPREHVQVTHNMPPQKEIPLDNLWVHLPKPEVKWPQDF 127	DR	
QY	-----	Query Match 87.7%; Score 1680; DB 1; Length 399; Best Local Similarity 87.1%; Pred. No. 3..1e-122; Mismatches 310; Conservative 29; Indels 0; Gaps 0;	
QY	-----	QY 8 SKEVENLKEFMPPEVHVQVTHNMPPQKEIPLDNLWVHLPKPEVKWPQDF 67 103 SKEVEISKKPPTPVPREVHLQVLSHMPQKIEFKMSMEDAQNLLHLDKVEKSMPQDF 103	
QY	-----	QY 68 LPDPASDGFDQVRLLERARELPLDYFVVLGDMITEALPLPTQTMNLNTLGVRDETGA	

		SQ	SEQUENCE	393 AA;	44857 MW;	C6A8788B8D8A0CC CRC64;	
Db	104	LDPASDGFFEDOVKELRERARELPDDYFVVLYGDMTEELALPTVQTMNLTGVRDETGA	163	Query Match	86.8%	Score 1662.5; DB 1; Length 393;	
Qy	128	SPTSWAIWTRAWTAEENRHGDLLNKLYLSSGRVMDRQEIKTQYLIGSGMDPRTEENSPYL	187	Best Local Similarity	85.7%	Pred. No. 6.7e-121;	
Db	164	SPTSWAVWTRAWTAEENRHGDLLNKLYLSSGRVMDRQEIKTQYLIGSGMDPRTEENNPL	223	Matches 311; Conservative	29;	Mismatches 22; Indels 1; Gaps 1;	
Qy	188	GFIYTSFQERATEFISHGNTARQAKEHGDIKLAQICGTIAADEKRHETAYTKIVKEKLFIED	247	Qy	1	ASTLKGSKVEVNKKPMPREHVQVTHSMPPQKIEIJKSLDNWAENTLVHLKPVEK 60	
Db	224	GFIYTSFQERATEFISHGNTARQAKEHGDIKLAQICGTIAADEKRHETAYTKIVKEKLFIED	283	Db	32	ASTVGPSTK-VETPKPMPREHVQVTHSMPPQKIEIJKSLDNWAENTLVHLKPVEK 90	
Qy	248	PGTVLAFADMMRKKSMPAHLYMGRDDNLFDHESSAVAQRQLGVYTAKDYADILEFLYGR	307	Qy	61	CWQPQDFLPDPSAGDGFDEQVRELRAKEIPDDYFVVLGDMITEALPYQTMLNTLG 120	
Db	284	PGTVVYAFADMMRKKSMPAHLYMGRDDNLFDNEFSSVAQRQLGVYTAKDYADILEFLAGR	343	Db	91	CWQPQDFLPDSSGEFGHEYKELRSKIEPDGYVYCLVSDMTIEALPYQTMLNTLG 150	
Qy	308	WKVDKLJTGLSAEGQKAQDYVGRPLPPIRLRERQAQCRAKEAPTMPESWIDRQVKL	363	Qy	121	VREDITGASPWSWAIWTRAWTAEENRHGDLLNKLYLSSGRVMDRQEIKTQYLIGSGMDPR 180	
Db	344	WRIESLTGSGEENKAQEYLGLTPRIRLDERAQRAKKGKPFWSWIDREVQL	399	Db	151	VRDETCASLTISWAWNRAWTAEENRHGDLLNKLYLSSGRVMDRQEIKTQYLIGSGMDPR 210	
RESULT 8				Qy	181	TENSPYLGFITYTSFQERATEFISHGNTARQAKEHGDIKLAQICGTIAADEKRHETAYTKIV 240	
SPAD_ELAGV		STANDARD;	PRT;	393 AA.	Db	211	TENSPYLGFITYTSFQERATEFISHGNTARQAKEHGDIKLAQICGTIAADEKRHETAYTKIV 270
TD	SPAD_ELAGV	STANDARD;	PRT;	393 AA.	Qy	241	EKLFEIDPDGTIVLAFAADMRRKKISMPAHLYMGRDDNLFDHFSAVQRLGVYTAKDYADI 300
AC	O24478				Db	271	EKLFEIDPDGTIVLSFADMKKKISMPAHLYMGRDDNLFEHSVAAQRGLGVDTAKDYADI 330
DT	15-DEC-1998	(Rel. 37, Created)			Qy	301	LEFLVGWRKVDKLTLGSLSEAGORAQDVYVCRLPPRIRLERAQGRAKEAPTMPSWIFDRQ 360
DT	15-DEC-1998	(Rel. 37, Last sequence update)			Db	331	LEFLINRWKVKGELTFSGEGKRAQDFVCTLAQPRIRRIERQERANKQAPRIPCSWLYGRE 390
DT	15-JUN-2002	(Rel. 41, Last annotation update)			Qy	361	VKL 363
DE	Acyl - acyl-carrier protein desaturase, chloroplast precursor				Db	391	VQL 393
DE	Acyl - acyl-carrier protein desaturase, chloroplast precursor						
OS	Elaeis guineensis var tenera (Oil palm)						
OC	Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; Spermatophytina; Magnoliophytina; Liliopsida; Arecoidae; Poales; Elaeidae; Elaeis; Elaeis						
OC	[1]						
RN	SEQUENCE FROM N.A.						
'RC	TISSUE-Mesocarp;						
RA	"Nucleotide sequence of a cDNA clone encoding stearoyl-acyl-carrier-						
RT	protein from Elaeis guineensis var tenera.";						
RL	(In) Plant Gene Register PGRE6-110.						
CC	-!- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL CHAIN.						
CC	-!- CATALYTIC ACTIVITY: Stearoyl-[acyl]-carrier protein + AH(2) + O(2) = oleoyl-[acyl]-carrier protein + A + 2 H(2)O.						
CC	-!- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.						
CC	-!- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE OILS.						
CC	-!- SUBUNIT: HOMODIMER (BY SIMILARITY).						
CC	-!- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF NONPHOTOSYNTHETIC TISSUES (BY SIMILARITY).						
CC	-!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.						
CC	-----						
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CC	EMBL: U68156; AAB41041.1; ALT_INIT.						
DR	HSSP; P22337; IAFER						
DR	InterPro; IPR005067; FA_desat.						
DR	InterPro; IPR01222; FA_desaturase.						
DR	Pfam: PF003405; FA_desaturase_2; 1.						
DR	PROSITE; PS00574; FATTY_ACID_DESATUR_2; 1.						
KW	Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast						
KW	Transit peptide.						
FT	TRANSIT CHAIN	31	CHLOROPLAST (BY SIMILARITY)				
FT	32	ACYL-[ACYL-CARRIER PROTEIN] DESATURASE					

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CC !- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.
 CC -! PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE OILS.
 CC
 DR !- SUBUNIT: HOMODIMER (BY SIMILARITY).
 DR !- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF NONPHOTOSYNTHETIC TISSUES (BY SIMILARITY).
 DR !- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
 CC
 DR This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and thus its statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC
 DR RMBL: X78935; CAAS55555.1; -.
 DR HSSP: P22337; IAFR.
 DR InterPro: IPR05067; FA_desat.
 DR InterPro: IPR01225; FA_Desaturase.
 DR Pfam: PF03405; FA_desatursase_2; 1.
 DR PROSITE: PS00574; FATTY_ACID_DESATURATE_2; 1.
 KW Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;
 KW Transit peptide.
 FT TRANSIT 1 33 CHLOROPLAST (BY SIMILARITY).
 FT CHAIN 34 396 ACYL-ACYL-CARRIER PROTEIN] DESATURASE.
 SQ SEQUENCE 396 AA; 45078 MW; 97E55A116791381 CRC64;

Query Match 86.4%; Score 1655; DB 1; Length 396;
 Best Local Similarity 86.5%; Pred. No. 2.6e-120;
 Matches 314; Conservative 19; Mismatches 30; Indels 0; Gaps 0;

1 ASTLKGSKEVENLKKPFMPBPREVHVQVTSMPPKIEIFKSLDNWAENILVHLKPVEK 60
 Db 34 ASTIGSATKVTESTKPKTPPREVHQVLISMPKQXIEKPSMEGAANNLVHLKPVEK 93
 Qy 61 CWQPODFLPDPAASDGDEQEVRLEBRAKEIPDDYFVVLGSDMITEALPYQTMLNTLG 120
 Db 94 CWQAQDFLPDPAASDGMEQEQLBLLRAKEIPDDYFVVLGSDMITEALPYQTMLNTLG 153
 Qy 121 VRDETQASPTSWAIWTRAWTAENRHGDLLNKLYLGSRVDMRQEFTIQYLIGSGMDPR 180
 Db 154 VRDETATLGLGVNTRAWTAENRHGDLLHQYLGSRVDMRQLQTKTQYLIGSGMDPR 213
 Qy 181 TENSPLYGFYTTSQERATFISHGNTARQAKEHGDIKLAQICGTIAADEKRHETAYTKIV 240
 Db 214 TENSPLYGFYTTSQERATFISHGNTARHAKEHGDVKLAQICGTIAADEKRHETAYTKIV 273
 Qy 241 EKLFEIDPDGTFLAFADMRRKTKISPAHLAAMDGRDNLFHDSAVAQRLGCVTTADYADI 300
 Db 274 EKLFEIDPDGTFLAFADMRRKTKISPAHLAAMDGRDNLFHDSAVAQRLGCVTTADYADI 333
 Qy 301 LEFLYGRWKVDKLTGLSAAQOKAQDYVCRLLPRIRRLEERAQGRAKEAPPMPFSWTFDQR 360
 Db 334 LEFLYGRWKVADLTGLESGERKAQDYVCGLAPRIRLEERSARAKESVNVPFSWTFDRE 393
 Qy 361 VKL 363
 Db 394 VKL 396

RESULT 10
 STAD_SOLCO
 ID STAD_SOLCO STANDARD: PRT; 393 AA.
 AC Q41379;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Acyl - acyl - carrier protein desaturase, chloroplast precursor
 DE Solanum commersonii (Commoner's wild potato).
 OS Eukaryota; Viridiplanteae; Streptophytina; Tracheophyta;
 OC Spermatophytina; Magnoliophytina; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
 OC NCBI_TaxID:4109;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE-Leaf;
 RA Truzzi M., Grillio S., Costa A., Leone A.;
 RA Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
 RL -! FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF A CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL CHAIN.
 CC DE Acyl - acyl - carrier protein desaturase, chloroplast precursor
 DE DE (EC 1.14.99.6) (Stearoyl-ACP desaturase).
 OS Olea europaea (Common Olive).
 CC = oleoyl-[acyl-carrier protein] + A + H(2)O.

OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
Asteridae	euasterids I; Lamiales; Oleaceae; Olea.		
NCBI_TaxID	4146;		
[1]	SEQUENCE FROM N.A.	RESULT 1.2	
STRAIN="CY; Leccino; TISSUE="Mesocarp;	STAD_SOLTU	STAD_SOLTU	
Baldoni L., Georgi L., Abbott A.G.;	ID	ID	
"Nucleotide sequence of a cDNA clone from <i>Olea europaea</i> encoding a	AC	P46253;	
stearoyl acyl carrier protein desaturase.";	DT	01-NOV-1995 (Rel. 32, Created)	
(In) Plant Gene Register PGR96 052.	DT	01-NOV-1995 (Rel. 32, Last sequence update)	
-!- FUNCTION: CONVERTS STEAROYL-ACP BY INTRODUCTION OF A	DT	15-JUN-2002 (Rel. 41, Last annotation update)	
CITS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL	DE	ACYL-1-acyl-carrier protein] desaturase, chloroplast precursor	
CHAIN.	DE	(EC 1.14.99.6) (Stearoyl-1-ACP desaturase).	
-!- CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + O(2)	OS	Beta-ketoacyl acyl-carrier protein desaturase, chloroplast precursor	
= oleoyl-[acyl-carrier protein] + A + 2 H(2)O.	OC	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
-!- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.	OC	Spermatozophores; Magnoliophyta; eudicotyledons; core eudicots;	
-!- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY	OC	Asteridae; euasterids I; Solanales; Solanaceae; Solanum.	
ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE	OX	NCBI_TaxID:4113;	
OILS.	RN		
-!- SUBUNIT: HOMODIMER (BY SIMILARITY).	RP	SEQUENCE FROM N.A.	
-!- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF	RA	Taylor M.A., Smith S.B., Davies H.V., Burch L.R.;	
NONPHOTOTSYNTHETIC TISSUES (BY SIMILARITY).	RL	"Nucleotide sequence of a cDNA clone from <i>Olea europaea</i> encoding a	
-!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.	CC	stearoyl acyl-carrier protein desaturase, chloroplast precursor".	
This SWISS-PROT entry is copyright. It is produced through a collaboration	CC	-!- FUNCTION: Converts STEAROYL-ACP to OLEOYL-ACP BY INTRODUCTION OF A	
between the Swiss Institute of Bioinformatics and the EMBL outstation -	CC	CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL	
the European Bioinformatics Institute. There are no restrictions on its	CC	CHAIN.	
use by non-profit institutions as long as its content is in no way	CC	CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + O(2)	
modified and this statement is not removed. Usage by and for commercial	CC	= oleoyl-[acyl-carrier protein] + A + 2 H(2)O.	
entities requires a license agreement (see http://www.isb-sib.ch/announce/	CC	-!- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.	
or send an email to license@isb-sib.ch).	CC	-!- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY	
ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE	CC	ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE	
OILS.	CC	ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE	
-!- SUBUNIT: HOMODIMER (BY SIMILARITY).	CC	OILS.	
-!- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF	CC	CC	
NONPHOTOTSYNTHETIC TISSUES (BY SIMILARITY).	CC	NONPHOTOTSYNTHETIC TISSUES (BY SIMILARITY).	
-!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.	CC	-!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.	
This SWISS-PROT entry is copyright. It is produced through a collaboration	CC	CC	
between the Swiss Institute of Bioinformatics and the EMBL outstation -	CC	CC	
the European Bioinformatics Institute. There are no restrictions on its	CC	CC	
use by non-profit institutions as long as its content is in no way	CC	CC	
modified and this statement is not removed. Usage by and for commercial	CC	CC	
entities requires a license agreement (see http://www.isb-sib.ch/announce/	CC	CC	
or send an email to license@isb-sib.ch).	CC	CC	
EMBL: U58141; AAB67940.1;	DR	CC	
HSSP: P22337; 1AFR.	DR	CC	
InterPro: IPR00567; FA_desat.	DR	CC	
InterPro: IPR001225; FA_desaturase.	DR	CC	
pfam: PF03405; FA_desaturation.	DR	CC	
PROSITE: PS00574; FATTY_ACID_DESATURASE_2; 1.	DR	CC	
Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;	DR	CC	
KW	DR	CC	
transit peptide.	DR	CC	
TRANSIT_1	FT	CC	
27	CHLOROPLAST (BY SIMILARITY).	CC	
28	ACYL-ACYL-CARRIER PROTEIN] DESATURASE.	CC	
SEQUENCE	FT	CC	
390 AA;	FT	CC	
44596 MW;	FT	CC	
39050E43ZB7AC2E3 CRC64;	FT	CC	
Score 1649; DB 1; Length 390;	QY	Query Match	
Best Local Similarity 85.1%; Pred. No. 7.3e-120;	QY	86.1%; Score 1626; DB 1; Length 393;	
Matches 309; Conservative 24; Mismatches 30;	Db	Best Local Similarity 82.4%; Pred. No. 4.4e-118;	
Indels 0; Gaps 0;	Db	Matches 299; Conservative 34; Mismatches 30; Indels 0; Gaps 0;	
	Db		
1 ASTLKGSKKEVENLKKPMPMPREHVQVTHSMPPKQIEFKSLDNWAENILVHLKPVEK 60	QY	1 ASTLKGSKKEVENLKKPMPMPREHVQVTHSMPPKQIEFKSLDNWAENILVHLKPVEK 60	
28 ASTHSPSMEVGKVKKPPTPREHVQVTHSLAPERIEINSNNWAENILVHLKDVK 87	Db	28 ASTHSPSMEVGKVKKPPTPREHVQVTHSLAPERIEINSNNWAENILVHLKDVK 87	
61 CWQPOQFLDPDASGDGEQVRERAREPAKTFPDYFVVLGDMITEBALPYQTMNLTDG 120	QY	61 CWQPOQFLDPDASGDGEQVRERAREPAKTFPDYFVVLGDMITEBALPYQTMNLTDG 120	
88 CWQPSFLPDSASSEGDEQMLRKCKETPDDYFVVLGDMITEBALPYQTMNLTDG 147	Db	88 CWQPSFLPDSASSEGDEQMLRKCKETPDDYFVVLGDMITEBALPYQTMNLTDG 147	
121 VRDETGAESPWSWAIINTRAWTAEENRGDLNKLYLGSRVDMRQIEKTIQYLGSGMDPR 180	QY	121 VRDETGAESPWSWAIINTRAWTAEENRGDLNKLYLGSRVDMRQIEKTIQYLGSGMDPR 180	
148 VRDETGASSLTPWAIINTRAWTAEENRGDLNKLYLGSRVDMQIEKTIQYLGSGMDPR 207	Db	148 VRDETGASSLTPWAIINTRAWTAEENRGDLNKLYLGSRVDMQIEKTIQYLGSGMDPR 207	
181 TENSPLYGLFITYSQRERATEFSHGNTAROAKEHGDIKLAQIGCTIAADEKRHETAYTKIV 240	QY	181 TENSPLYGLFITYSQRERATEFSHGNTAROAKEHGDIKLAQIGCTIAADEKRHETAYTKIV 240	
208 TENVPLYGLFITYSQRERATEFSHGNTARLAKETHGDIKLAQIGCTIAADEKRHETAYTKIV 267	Db	208 TENVPLYGLFITYSQRERATEFSHGNTARLAKETHGDIKLAQIGCTIAADEKRHETAYTKIV 267	
241 EKLFELDPDGTVLAFADMRRKKIISMPAHMLYGRDNLEDFHSAYAQLRGYTTAKYADI 300	QY	241 EKLFELDPDGTVLAFADMRRKKIISMPAHMLYGRDNLEDFHSAYAQLRGYTTAKYADI 300	
268 LEFLFLDPGVWLAJADMMRKVYSMAHMLYGRDNLEDFHSAYAQLRGYTTAKYADI 327	Db	268 LEFLFLDPGVWLAJADMMRKVYSMAHMLYGRDNLEDFHSAYAQLRGYTTAKYADI 327	
301 LEFLFLRGWKVDTLGLSAQGQAQDYCRLLPPIRRLERERAGRAKEAPTMPSWIFDPR 360	QY	301 LEFLFLRGWKVDTLGLSAQGQAQDYCRLLPPIRRLERERAGRAKEAPTMPSWIFDPR 360	
328 LEFLFLRGWDIEKLTLGTLGSSEGRRKAQDYVCTLPPIRRLERERAGSRVKKASATPSWIFGRE 387	Db	328 LEFLFLRGWDIEKLTLGTLGSSEGRRKAQDYVCTLPPIRRLERERAGSRVKKASATPSWIFGRE 387	
361 VKL 363	QY	361 VKL 363	

DR	EMBL; M83199; AAA33932.1; -.	CC	-1 - PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE OILS.
DR	InterPro; P22337; IAFR.	CC	-1 - SUBUNIT: HOMODIMER (BY SIMILARITY).
DR	InterPro; IPR00567; FA_desat.	CC	-1 - SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS OF NONPHOTOSYNTHETIC TISSUES (BY SIMILARITY).
DR	InterPro; IPR00125; FA_desaturase.	CC	-1 - SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
DR	PS00574; Fatty_Acid_DESATUR_2; 1.	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
KW	Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;	CC	
KW	Transit peptide.	CC	
FT TRANSIT	1 34 CHLOROPLAST (BY SIMILARITY)	CC	
FT CHAIN	1 35 398 Amino acids MW: 45130 CRC64;	CC	
SEQ	398 AA: F3E00BB04427DB	CC	
Query Match	Score 83.9% Length 398;	DR	HSSP; P22337; IAFR.
Best Local Similarity	83.9% Pred. No. 1; 3e-16;	DR	InterPro; IPR00567; FA_desat.
Matches 297; Conservative 33; Mismatches 33; Indels 0; Gaps 0;	DR	InterPro; IPR00125; FA_desaturase.	
QY 1 ASTLKGSGKEVENLKKPFMPREHVQVTHSPQQKLEIFKSLDNWAENILVHLKPEK 60	DR	Prosite; PS00574; Fatty_Acid_DESATUR_2; 1.	
Db 36 SSTIGTSKEIPNAKKHMPPREAHQVTKHNSPPQKTEIFKSLLEGMAEENVVLVHLKPEK 95	DR	ACYL-[ACYL-CARRIER PROTEIN] DESATURASE.	
QY 61 CWPQDFLPDPASDGFDEQVRERERAKEIIPDDYFVVLVGDMITEEALPTYCTQMLNLTLDG 120	DR	CHLOROPLAST (BY SIMILARITY).	
Db 96 CWPQDFLPDPASGFMDQVKERERAKIPEVLYLVGDNITEEALPTYCTQMLNLTLDG 155	DR	Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast.	
QY 121 VDETGTASPTSAIWIWTRAWTAENRHGDLLNRYYLGSRVMDMROIETKTIVQLIGSGMDPR 180	FT	Transit peptide.	
Db 156 VDETGTASLTSAIWIWTRAWTAENRHGDLLNRYYLGSRVMDMROIETKTIVQLIGSGMDPR 215	FT	CHAIN 1 31 CHLOROPLAST (BY SIMILARITY).	
QY 181 TENSPLYGLFIYTSQERATFISHGNTARQAKEHDIKLAQIQTGTTIADEKRHETAYTKIV 240	FT	CHAIN 32 ASTLKGSGKEVENLKKPFMPREHVQVTHSPQQKLEIFKSLDNWAENILVHLKPEK 60	
Db 216 SENNPYGLFIYTSQERATFISHGNTARLAKHGDFLQAVQCGITADEKRHETAYTKIV 275	FT	SEQUENCE 32 ASTLKGSGKEVENLKKPFMPREHVQVTHSPQQKLEIFKSLDNWAENILVHLKPEK 87	
QY 241 EKLFIEIDPDGTIVLAFADMIRKKTISMPAHMLYGRDDNLFDHESAVAGRLGYTTAKDYADI 300	FT	QY 1 ASTLKGSGKEVENLKKPFMPREHVQVTHSPQQKLEIFKSLDNWAENILVHLKPEK 60	
Db 276 EKLFIEIDDGAVLALADMIRKKTISMPAHMLYGRDDNLFDHESAVAGRLGYTTAKDYADI 335	FT	DB 32 ASTLKGSGKEVENLKKPFMPREHVQVTHSPQQKLEIFKSLDNWAENILVHLKPEK 87	
QY 301 LEFLVGRMKVKDILTGLSAEGKAQDYVCRLPRTRIRLEERAQRAKEBAPTMSWIFDRO 360	FT	QY 61 CWPQDFLPDPASDGFDEQVRERERAKEIIPDDYFVVLVGDMITEEALPTYCTQMLNLTLDG 120	
Db 336 LEHLVNROKVNENGLSSEGHIAQDFVCGLAPRKGERAANSLSKPVSLSVFSWIFNE 395	FT	DB 88 SWPQDFLPDPASDGFDEQVRERERAKEIIPDDYFVVLVGDMITEEALPTYCTQMLNLTLDG 147	
QY 361 VKL 363	FT	QY 121 VDETGTASPTSAIWIWTRAWTAENRHGDLLNRYYLGSRVMDMROIETKTIVQLIGSGMDPR 180	
Db 396 LKV 398	FT	DB 148 VDETGTASPTWAWTRAWTAENRHGDLLNRYYLGSRVMDMROIETKTIVQLIGSGMDPG 207	
RESULT 15	FT	QY 181 TENSPLYGLFIYTSQERATFISHGNTARQAKEHDIKLAQIQTGTTIADEKRHETAYTKIV 240	
ID STAD_ORYSA STANDARD; PRT; 390 AA.	FT	DB 208 TENNPYGLFIYTSQERATFISHGNTARQAKEHDIKLAQIQTGTTIADEKRHETAYTKIV 267	
AC 31; DT 15-DEC-1998 (Rel. 37, Created)	FT	QY 241 EKLFIEIDPDGTIVLAFADMIRKKTISMPAHMLYGRDDNLFDHESAVAGRLGYTTAKDYADI 300	
DT 15-DEC-1998 (Rel. 37, Last sequence update)	FT	DB 268 EKLFIEIDPDGTIVLAFADMIRKKTISMPAHMLYGRDDNLFDHESAVAGRLGYTTAKDYADI 327	
DE Acyl-[acyl-carrier protein] desaturase, chloroplast precursor (EC 1.14.99.6) (Stearoyl-ACP desaturase).	FT	QY 301 LEFLVGRMKVKDILTGLSAEGKAQDYVCRLPRTRIRLEERAQRAKEBAPTMSWIFDRO 360	
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.	FT	DB 328 LEFLVGRMKVKDILTGLSAEGKAQDYVCRLPRTRIRLEERAQRAKEBAPTMSWIFDRO 387	
OC NCBI_TAXID=4530; ORX [1]	FT	QY 361 VKL 363	
RN SEQUENCE FROM N. A.	FT	DB 388 VQL 390	
RC STRAIN=cv. Nipponbare; TISSUE=Seed; MEDLINE=95334510; PubMed=7610181; RA Akagi H., Baba T., Shimada H., Fujimura T.; RT "Nucleotide sequence of a stearoyl-acyl carrier protein desaturase cDNA from developing seeds of rice."; RL Plant Physiol. 108:845-846 (1995).	FT	Search completed: March 7, 2003, 03:09:10 Job time : 15 secs	
CC -!- FUNCTION: Converts Stearoyl-ACP to Oleoyl-ACP by introduction of a cis double bond between carbons delta-9 and delta-10 of the acyl chain.	FT		
CC -!- CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + O(2) = oleoyl-[acyl-carrier protein] + A + 2 H ₂ O.	FT		
CC -!- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.	FT		

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OM protein - protein search, using sw model

Run on: March 7, 2003, 03:07:27 : Search time 22 Seconds

(without alignments)
1586.218 Million cell updates/sec

Title: US-10-017-145-1

Perfect score: 1916

Sequence: 1 ASTLKGSKKEVNLKKPFMP RAKEAPTMPFSWIFDRQVKL 363

Scoring table: BLOSUM62

Gappen 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters:

283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

PIR:73-*

1: Pir1,*

2: Pir2,*

3: Pir3,*

4: Pir4,*

RESULT 1

OHCSAD

acyl-acyl-carrier-protein]

desaturase (EC 1.14.19.2)

precursor - castor bean

N; Alternate names:

stearoyl-[acyl-carrier-protein]

desaturase

C; Species:

Ricinus communis

(castor bean)

C; Date:

31-Dec-1992

#sequence_change

03-Jun-2002

C; Accession:

S16463; A39170

R; Knutzon, D.S.; Scherer, D.E.; Schreckengost, W.E.

Plant Physiol.

96,

344-345;

1991

A; Title:

Nucleotide

sequence of a complementary DNA clone encoding stearoyl-acyl car-

A; Reference number:

S16463

A; Accession:

S16463

A; Molecule type: mRNA

A; Residues: 1-396 <KNU>

A; Cross-references: EMBL:X56508; PID:921092; PMID:CAA39859.1; PID:921093

R; Shanklin, J.; Somerville, C.

Proc. Natl. Acad. Sci. U.S.A.

88,

2510-2514;

1991

A; Title:

stearoyl-acyl-carrier protein desaturase from higher plants is structurally

A; Reference number:

A39170

A; Status: preliminary

A; Molecule type: mRNA

A; Residues: 1-396 <SHA>

A; Cross-references: GB:M58588

A; Note: parts of this sequence were confirmed by peptide sequencing

C; Superfamily:

acyl-acyl-carrier protein

desaturase

C; Keywords:

chloroplast; fatty acid biosynthesis; oxidoreductase

F; 1-31/Domain:

transit peptide (chloroplast)

#status predicted <NP>

F; 34-396/Product:

acyl-acyl-carrier protein]

desaturase #status predicted <MAT>

Query Match

100.0%

Score: 1916;

DB 1;

Length: 396;

Best Local Similarity

100.0%;

Pred. No.

0;

Mismatches

0;

Indels

0;

Gaps

0;

Matches

363;

Conservative

0;

Differences

0;

Insertions

0;

Deletions

0;

Inversions

0;

Reversals

0;

Splices

0;

Frameshifts

0;

Terminators

0;

Startsites

0;

Stopsites

0;

Introns

0;

Exons

0;

Splicing

0;

Termination

0;

Start

0;

Stop

0;

Intron

0;

Exon

0;

Splice

0;

Terminator

0;

Startsite

0;

Stopsite

0;

Intronsite

0;

Exonsite

0;

Splicing

0;

Termination

0;

Startsite

0;

Stopsite

0;

Intronsite

0;

Exonsite

0;

Splicing

0;

Termination

0;

Startsite

0;

Stopsite

0;

Intronsite

0;

Exonsite

0;

Splicing

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Termination

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Startsite

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Stopsite

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Intronsite

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Exonsite

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Splicing

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Termination

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Startsite

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Stopsite

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Intronsite

0;

Exonsite

0;

Splicing

0;

Termination

0;

Startsite

0;

Stopsite

0;

Intronsite

0;

Exonsite

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Splicing

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Termination

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1318 68.8 374 2 A96502

1317 68.7 385 2 A47245

22 307 16.0 328 2 T35035

23 272 14.2 338 2 H70810

24 267 13.9 338 2 D87182

25 158 8.2 275 2 C87153

26 138 7.2 375 2 D70896

27 112.5 5.9 389 2 D82223

28 112.5 5.9 1155 2 G87477

29 108 5.6 744 2 T09541

hypothetical protein

DNA (cytosine-5')-

ATP-dependent CLP

endopeptidase clpB

hypothetical protein

probable polyketid

367 K tagment prot

probable nuclear prote

ribonucleoside-diph

ribonucleoside-diph

oligoendopeptidase

oligoendopeptidase

146D nuclear prote

146D nuclear prote

hypothetical protein

ribonucleoside-diph

		A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-396 <TH0>
QY	301 LEPFLVGRWKVDKUTLGTLGSAEGOKAQDVCRLPPRIRLEERAQGRAKEAAPTMPFSWIFDRO 360	A; Cross-references: GB:M61109; NID:9167196; PID:AAA33021.1; PID:9167197
Db	334 LEPFLVGRWKVDKUTLGTLGSAEGOKAQDVCRLPPRIRLEERAQGRAKEAAPTMPFSWIFDRO 393	C; Superfamily: acyl-[acyl-carrier-protein] desaturase C; Keywords: chloroplast; oxidoreductase
QY	361 VKL 363	
Db	394 VKL 396	
		Query Match 91.4%; Score 1752; DB 1; Length 396; Best Local Similarity 90.1%; Pred. No. 1..6e-12.; Indels 0; Gaps 0;
		Matches 327; Conservative 18; Mismatches 18; Gaps 0;
		Query 1 ASTLKGSGKEVENLKKPMPREPVHQVTHSMPPQKIEFKSVDNAEENTLVHLKPVEK 60
QY	1 ASTLKGSGKEVENLKKPMPREPVHQVTHSMPPQKIEFKSVDNAEENTLVHLKPVEK 60	
Db	34 ASTLGSSTPKVDNAKKFPQPBPVHQVTHSMPPQKIEFKSIEGMAQNLYHLKPVEK 93	
		Query 61 CWQOPQDFLPDPASDGFPEQVRLERAKIEPDYFVVLGDMITEALPTVOTMLNLTLDG 120
QY	61 CWQOPQDFLPDPASDGFPEQVRLERAKIEPDYFVVLGDMITEALPTVOTMLNLTLDG 120	
Db	94 CWQQAQDFLPDPASGEFDQVKDLRAREKIEPDYFVVLGDMITEALPTVOTMLNLTLDG 153	
		Query 121 VRDETAGSPSWAIWTRAWTAENRHGDLNKYLGLSGRVDMRQ1EKTIQVLLIGSGMDPR 180
QY	121 VRDETAGSPSWAIWTRAWTAENRHGDLNKYLGLSGRVDMRQ1EKTIQVLLIGSGMDPR 180	
Db	154 VRDETAGSPSWAIWTRAWTAENRHGDLNKYLGLSGRVDMRQ1EKTIQVLLIGSGMDPR 180	
		Query 154 VRDETAGSPSWAIWTRAWTAENRHGDLNKYLGLSGRVDMRQ1EKTIQVLLIGSGMDPR 180
QY	154 VRDETAGSPSWAIWTRAWTAENRHGDLNKYLGLSGRVDMRQ1EKTIQVLLIGSGMDPR 180	
Db	154 VRDETAGSPSWAIWTRAWTAENRHGDLNKYLGLSGRVDMRQ1EKTIQVLLIGSGMDPR 180	
		Query 181 TENSPYLGFIYTFSQERATEFISHGNTARQAEHGDIKLAQICGTIADEKRHETATKIV 240
QY	181 TENSPYLGFIYTFSQERATEFISHGNTARQAEHGDIKLAQICGTIADEKRHETATKIV 240	
Db	214 TENSPYLGFIYTFSQERATEFISHGNTARQAEHGDIKLAQICGTIADEKRHETATKIV 240	
		Query 214 TENSPYLGFIYTFSQERATEFISHGNTARQAEHGDIKLAQICGTIADEKRHETATKIV 240
QY	214 TENSPYLGFIYTFSQERATEFISHGNTARQAEHGDIKLAQICGTIADEKRHETATKIV 240	
Db	214 TENSPYLGFIYTFSQERATEFISHGNTARQAEHGDIKLAQICGTIADEKRHETATKIV 240	
		Query 241 EKLFEIDPDGTYLAFADMRRKKTISMPAHLM/DGRDDNLFIDHSAVAGRLGYYTAKDADI 300
QY	241 EKLFEIDPDGTYLAFADMRRKKTISMPAHLM/DGRDDNLFIDHSAVAGRLGYYTAKDADI 300	
Db	274 EKLFEIDPDGTYLAFADMRRKKTISMPAHLM/DGRDDNLFIDHSAVAGRLGYYTAKDADI 333	
		Query 301 LEFLVGGRWKVDKLTGTLGSAEGOKAQDVFQLPPIRRLERAKIEQGRAKEAAPTMPFSWIFDRO 360
QY	301 LEFLVGGRWKVDKLTGTLGSAEGOKAQDVFQLPPIRRLERAKIEQGRAKEAAPTMPFSWIFDRO 360	
Db	334 LEFLVGGRWKVDKLTGTLGSAEGOKAQDVFQLPPIRRLERAKIEQGRAKEAAPTMPFSWIFDRO 393	
		RESULT 4
		T07806 acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) precursor - soybean
		N; Alternative names: stearoyl-acyl carrier protein desaturase
		C; Species: Glycine max (soybean)
		C; Date: 14-May-1999 #sequence_revision 14-May-1999 *text_change 03-Jun-2002
		R; Chen, B.Y.; Janes, H.W.
		Submitted to the EMBL Data Library, July 1994
		A; Reference number: 216145
		A; Accession: T07806
		A; Status: preliminary; translated from GB/EMBL/DBJ
		A; Molecule type: mRNA
		A; Residues: 1-411 <CHE>
		C; Genetics:
		A; Gene: SACPD
		A; Genome: nuclear
		C; Superfamily: acyl-[acyl-carrier-protein] desaturase
		C; Keywords: Chloroplast; oxidoreductase
		F; 1-29/Domain: transit peptide (chloroplast) #status predicted <TNP>
		Query Match 90.7%; Score 1738; DB 2; Length 411;
		Best Local Similarity 89.4%; Pred. No. 1..9e-123; Mismatches 13; Indels 0; Gaps 0;
		Matches 322; Conservative 25; Mismatches 13; Gaps 0;
		Query 1 ASTLKGSGKEVENLKKPMPREPVHQVTHSMPPQKIEFKSVDNAEENTLVHLKPVEK 60
QY	1 ASTLKGSGKEVENLKKPMPREPVHQVTHSMPPQKIEFKSVDNAEENTLVHLKPVEK 60	
Db	29 ASTLRSGGSKKEVENIKKPKTPPPREPVHQVTHSMPPQKIEFKSVDNAEENTLVHLKPVEK 88	
		Query 61 CWQOPQDFLPDPASDGFPEQVRLERAKIEPDYFVVLGDMTEALPTVOTMLNLTLDG 120
QY	61 CWQOPQDFLPDPASDGFPEQVRLERAKIEPDYFVVLGDMTEALPTVOTMLNLTLDG 120	
Db	89 CWQOPQDFLPDPSSSDGFEEQVKLERAKELPDDYFVVLGDMTEALPTVOTMLNLTLDG 148	
		A; Reference number: A39173; MUID:91172850; PMID:2006194
		A; Reference number: A39173; MUID:91172850; PMID:2006194

Qy	121	VRDETGASPTSWAIWTRAWTAEEENRHGDLNKLYLIGSGMDPR	180	C;Species: Helianthus annuus (common sunflower) C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002
Db	149	VRDETGASLTSWAIFTRAWTAEEENRHGDLNKLYLIGSGMDPR	208	C;Accession: T14264 R;Hongtrakul, V.; Slabaugh, M.B.; Knapp, S.J. submitted to the EMBL Data Library, February 1997 A;Description: Sunflower Stearyl-ACP desaturase. A;Reference number: Z17946 A;Status: preliminary; translated from GB/EMBL/DDJB
Qy	181	TENSPYLGFYTSFQERATFISHGNTAROKEHGDIKLAQICCTIAADEKRHETAYTKIV	240	A;Molecule type: mRNA A;Residues: 1-396 <HON> A;Cross-references: EMBL:U91339; NID:92290399; PID:g2290400
Db	209	TENSPYLGFYTSFQERATFISHGNTARLAKEHGDIKLAQICGMIAESDKRHETAYTKIV	268	A;Experimental source: strain Mammoth C;Function: A;Description: introduces a double bond at the delta(9) position of stearoyl-ACP gene C;Superfamily: acyl [acyl-carrier-protein] desaturase C;Keywords: fatty acid biosynthesis; oxido-reductase
Qy	241	EKLEIDPGTVALFADMMRKKSMPAHMLYMDGRDDNLFDHSSVAQRQLGVITAKDYADI	300	Query Match Score 90.1%; Score 1727; DB 2; Length 396; Best Local Similarity 88.7%; Pred. No. 1.2e-122; Matches 322; Conservative 23; Mismatches 18; Indels 0; Gaps 0;
Db	269	EKLEIDPGTVMADMMRKKTAMPAHMLYMDGRDDNLFDHSSVAQRQLGVITAKDYADI	328	Qy 1 ASTIJKSKEVENLKKPFMPPREVTHSMPPQTIEFERSLDNWAENILVHLKPVEK 60 Db 34 ASTIJSSTPKVESTKPKFTPREVHLQVTHSMPPQTIEKTSIEGMAEDNLVHLKPVEK 93
Qy	301	LEFLVGWKDQKLTGSAEGLQADQYVCPLLPRLERAAQRAKEAPTMPSWIFDRQ	360	Qy 61 CWQPODFLPDPASDGFQYRELREFRAKEIPLDDYFVVLGVDMITEALPYQTMLNTLDG 120 Db 94 CWQPODFLPPEASDGFEEQYKELRRAKEIPLDEYFVVLGVDMITEALPYQTMLNTLDG 153
Db	329	LEFLVGWRKWKVEQINTGLSGEGRKAQEYICGLPPRIRLERAAQRAVKESTLKFWSWHDRE	388	Qy 121 VRDEENGASPTSWAIWTRAWTAEEENRHGDLNLKLYLIGSGMDPR 180 Db 154 VRDEENGASPPWATRANTAAEENRHGDLNLKLYLIGSGMDPR 213
<hr/>				
RESULT 5				
Qy	84869	stearoyl-ACP desaturase [imported] - Arabidopsis thaliana	0	C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
Db	84869	stearoyl-ACP desaturase [imported] - Arabidopsis thaliana	0	C;Accession: E84869 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Talion, L.; euss, D.; Nievergelt, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venier, J.; Nature 402, 761-768, 1999 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; PMID:20083487; PMID:10617197 A;Accession: E84869 A;Status: preliminary A;Residues: 1-401 <STO> A;Cross-references: GB:AE002093; NID:92281099; PID:gN00139
Db	84869	stearoyl-ACP desaturase [imported] - Arabidopsis thaliana	0	C;Genetics: A;Gene: At2g43710 A;Map position: 2 C;Superfamily: acyl-[acyl-carrier-protein] desaturase
Qy	4	LKSGSKKEVENLKKPFMPPREVHYQVOTHSMPPQTIEFISLDDNWAENILVHLKPVEKCWQ	63	Query Match Score 90.4%; Score 1733; DB 2; Length 401; Best Local Similarity 89.4%; Pred. No. 4.3e-123; Matches 322; Conservative 22; Mismatches 22; Indels 0; Gaps 0;
Db	42	LSSGPKEVELSKKPFPTPPREVHYQVOTHSMPPQTIEFISLDDNWAENILVHLKPVEKCWQ	101	Qy 64 PQQDFLPDPASDGFQDEVRLERAKELPDIYFVVLGVDMITEALPYQTMLNTLDGYRD 123 Db 102 PQQDFLPDPASDGFQEVRLERAKELPDIYFVVLGVDMITEALPYQTMLNTLDGYRD 161
Qy	124	ETGASPTSWAIWTRAWTAEEENRHGDLNKLYLIGSGMDPR	183	Qy 124 ETGASPTSWAIWTRAWTAEEENRHGDLNKLYLIGSGMDPR Db 162 ETGASPTSWAIWTRAWTAEEENRHGDLNKLYLIGSGMDPR
Db	162	ETGASPTSWAIWTRAWTAEEENRHGDLNKLYLIGSGMDPR	221	N;Alternate names: stearoyl-[acyl-carrier-protein] desaturase C;Species: Spinacia Oleracea (spinach) C;Accession: S22480; S18183 R;Nishida, I.; Beppu, T.; Matsuura, T.; Murata, N.
Qy	184	SPYLGFYTSFQERATFISHGNTAROKEHGDIKLAQICCTIAADEKRHETAYTKIVEKL	243	C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 03-Jun-2002
Db	222	NPYLGFYTSFQERATFISHGNTAROKEHGDIKLAQICCTIAADEKRHETAYTKIVEKL	281	Qy 244 FEIDPDGTVALFADMMRKKSMPAHMLYMDGRDDNLFDHSSVAQRQLGVYTAKDYADILEF 303 Db 282 FEIDPDGTVALFADMMRKKSMPAHMLYMDGRDNLFEDNEFSSVAQRQLGVYTAKDYADILEF 341
Qy	304	LVGRKVKDQKLTGSAEGLQADQYVCPLLPRLERAAQRAKEAPTMPSWIFDRQVKL	363	Qy 304 LVGRKVKDQKLTGSAEGLQADQYVCPLLPRLERAAQRAKEAPTMPSWIFDRQVKL 363 Db 342 LVGRKVKDQKLTGSGEGNKAQDYLGLGAPLKRLDERAAQRAKKGPKIFPSWHDREVQL 401
<hr/>				
RESULT 6				
Qy	14264	acyl-acyl-carrier-protein] desaturase (EC 1.14.19.2) - common sunflower	0	N;Alternate names: stearoyl-ACP desaturase
Db	14264	acyl-acyl-carrier-protein] desaturase (EC 1.14.19.2) - common sunflower	0	R;Hongtrakul, V.; Slabaugh, M.B.; Knapp, S.J. submitted to the EMBL Data Library, February 1997 A;Description: Sunflower Stearyl-ACP desaturase. A;Reference number: Z17946 A;Status: preliminary; translated from GB/EMBL/DDJB
Qy	342	acyl-acyl-carrier-protein] desaturase (EC 1.14.19.2) - common sunflower	0	A;Molecule type: mRNA A;Residues: 1-39 <NTS> A;Cross-references: EMBL:X62898; NID:921229; PID:g21230 C;Superfamily: acyl-acyl-carrier-protein] desaturase C;Keywords: chloroplast; fatty acid biosynthesis; oxidoreductase F;1-3/Domain: transit peptide (chloroplast) #status predicted <MAT>
Db	342	acyl-acyl-carrier-protein] desaturase (EC 1.14.19.2) - common sunflower	0	Query Match Score 90.0%; Score 1724.5; DB 1; Length 399; Best Local Similarity 87.9%; Pred. No. 1.9e-122;

A; Accession: S24995 A; Molecule type: mRNA A; Residues: 1-99 <SLO> A; Cross-references: EMBL:X63304; NID:917869; PID:CAA4964..1; PID:917870 C; Superfamily: acyl [acyl]-carrier protein desaturase C; Keywords: chloroplast; fatty acid biosynthesis; homodimer; oxidoreductase	Query Match Score 87.7%; Best Local Similarity 87.1%; Matches 310; Conservative 29; Mismatches 17; Indels 0; Gaps 0;	Qy 8 SKEVENLKPKEMPMPREHYDOTHSMPPKOKIEFKSLDNNAEENILVHLKPKVEKCWQPQDF 67 Db 44 SKEVELSKKPFETPPEVHLQVLSMPKQKTEIFKSMEDRAEQNLLPHLKVEKSWQPQDF 103
		Qy 68 LPDPASDGFEQEVRLERKEIPTDYFVYLVGDMITEALPLPTQTMNLTLDGYRDETA 127 Db 104 LPDPASDGFEQEVRLERKEIPTDYFVYLVGDMITEALPLPTQTMNLTLDGYRDETA 163
		Qy 128 SPTSAWIWTAWATAEENRHQDLNLKYPLSGRVDMRQIENTQLIGSGMDPRINPSVY 187 Db 164 SPTSAWIWTAWATAEENRHQDLNLKYPLSGRVDMRQIENTQLIGSGMDPRINPSVY 223
		Qy 188 GFITYTSFQERATEISHGNTARQAKEHGDIKLAQICGTIAADEKRHETAYTKEVKEFLIED 247 Db 224 GFITYTSFQERATFVSHGNPQTARQAKEHGDLKLAQICGTIAADEKRHETAYTKEVKELEID 283
		Qy 248 PDGTVLAFADEMRKKISMPAHLYMDGRDDNLFDHESAVAQRLGVYTAKDYADILEFLYGR 307 Db 284 PDGTVVAFADEMRKKISMPAHLYMDGRDDNLFDHESAVAQRLGVYTAKDYADILEFLAGR 343
		Qy 308 WKVDKLTKLGSAGEGOKAQDYZCRLPPTRIRLEERAQKPAEPTMPFSWIDRQYKL 363 Db 344 WRIESLTGSGEGNKAQAEYLCGLTPIRRLDERAQARAKGPKIPFSWIHDREVQI 399
RESULT 11		
* S71264 acyl - acyl-carrier-protein] desaturase (EC 1.14.19.2) - Arabidopsis thaliana C; Species: Arabidopsis thaliana. (mouse ear cress) C; Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 03-Jun-2002 C; Accession: S71264 R; Piffanelli, P.; Murphy, D.J. submitted to the EMBL Data Library, November 1995 A; Description: Cloning of a stearoyl-ACP desaturase from Arabidopsis thaliana. A; Reference number: S71264 A; Molecule type: mRNA A; Cross-references: EMBL:X93461; NID:91107506; PID:CAA63746..1; PID:91107507 C; Superfamily: acyl [acyl]-carrier protein desaturase C; Keywords: fatty acid biosynthesis; oxidoreductase	Query Match Score 86.7%; Best Local Similarity 87.9%; Matches 311; Conservative 21; Mismatches 17; Indels 5; Gaps 1;	Qy 4 LKGSKVEENLKKPKMPMPREHYDOTHSMPPKQKIEFKSLDNNAEENILVHLKPKVEKCMQ 63 Db 42 LSSGPREVEEKKPKTPPREHYQVLHSMPKQKIEFKSLDNNAEENILVHLKPKVEKSMQ 101
		Qy 64 PQDFLPDPASDGFEQVRERAREAKEIPDDYFVVLGDMTEALPLTYQMLNLTLDGVRD 123 Db 102 PQDFLPDPASDGFEQVRERAREAKEIPDDYFVVLGDMTEALPLTYQMLNLTLDGVRD 161
		Qy 124 ETGASPTSWAIWTAWATAEENRHQDLNLKYPLSGRVDMRQIENTQLIGSGMDPRINPSVY 183 Db 162 ETGASPTSWAIWTAWATAEENRHQDLNLKYPLSGRVDMRQIENTQLIGSGMDPRINPSVY 221
		Qy 304 LVGRWKVDKLTKLGSAGEGOKAQDYZCRLPPTRIRLEERAQKPAEPTMPFSWIDRQ 360 Db 342 LVGRWKVDKLTKLGSAGEGOKAQDYZCRLPPTRIRLEERAQKPAEPTMPFSWIDRQ 393
RESULT 13		
S44202 acyl - acyl-carrier-protein] desaturase (EC 1.14.19.2) precursor - Commerson's wild potato C; Alternate names: stearoyl-ACP desaturase C; Species: Solanum commersonii (Commerson's wild potato) C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 03-Jun-2002 C; Accession: S44202	Qy 184 SPYLGFIYTSFQERATFISHGNTARQAKEHGDIKLAQICCTIAADEKRHETAYTKEVKL 243 Db 222 NPYLGFIYTSFQERATFISHGNTARQAKEHGDIKLAQICCTIAADEKRHETAYTKEVKL 281	

R;Trucci, M.; Grillo, S.; Costa, A.; Leone, A.
Submitted to the EMBL Data Library, April 1994
A;Reference number: S44202
A;Molecule type: mRNA
A;Residues: 1-393 <TRU>
A;Cross-references: EMBL:X78935; NID:9474832; PIDN:CAA55535.1; PID:9474833
C;Genetics:
A;Genome: nuclear
C;Superfamily: acyl-[acyl]-carrier protein desaturase
C;Keywords: chloroplast; fatty acid biosynthesis; oxidoreductase
F;1-30/Domain: transit peptide (chloroplast) #status predicted <TP>
F;31-393/Product: acyl-[acyl-carrier-protein] desaturase #status predicted <MAT>

Query Match 86.2%; Score 1652; DB 2; Length 393;
Best Local Similarity 84.8%; Pred. No. 5.4e-117;
Matches 308; Conservative 24; Mismatches 31; Indels 0; Gaps 0;

Qy 1 ASTLKSGSKVEVNLRKPFMPREHVQVTHSMPPQKIEFKSLDNWAEEENILVHLKPVEK 60
Db 31 ASTHRSPEVGSKKAFTPPREHVQVTHSMPPKIEFKSLDNWAANLLVHLKPVEK 90

Qy 61 CWQPDFLPDPASDGFDEQYRELRAKEIPDDYFVVLVGDMDTTEALPTYQTMNLTDG 120
Db 91 CWQPDFLPDPASDGFDEQYRELRAKEIPDDYFVVLVGDMDTTEALPTYQTMNLTDG 150

Qy 121 VDETGAQPTSWAIWTRATAEENRGDLNLKLYLSGRVDMRQIEKTQYLIGSGMDPR 180
Db 151 VDETGAQPTSWAIWTRATAEENRGDLNLKLYLSGRVDMRQIEKTQYLIGSGMDPR 210

Qy 181 TENSPLYGLTYSQERATFISHGNTARQAKHGDIKLAQICGTIAADEKRHETAYTKIV 240
Db 211 TENNPHLGFIYTYSQERATFISHGNTARHAKHGDIMKLAQVGTTIAADEKRHETAYTKIV 270

Qy 241 EKLEFIDPDGTVALAFADMRKKSIMPALMYGDRDDNLFDHFSAVQLGVYTAKDYADI 300
Db 271 EKLEFIDPDGTVALADMRKKSIMPALMYGDRDDNLFEHFSAVQLGVYTAKDYADI 330

Qy 301 LEFLVGRKVKDKLTGLSSEGOKAQDYVCRLPPRIRRLERAGRAKEAPTMPSWIFRQ 360
Db 331 LEFHGRNEVEKLTGSSGRRAQDYVCGLAPRKLEERAQAKHAKSVPSWIFRQE 390

Qy 361 VKL 363
Db 391 IKL 393

RESULT 15
T10793
acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) precursor - upland cotton
Db 211 TENNPHLGFIYTYSQERATFISHGNTARHAKHGDIMKLAQVGTTIAADEKRHETAYTKIV 270
Qy 241 EKLEFIDPDGTVALAFADMRKKSIMPALMYGDRDDNLFDHFSAVQLGVYTAKDYADI 300
Db 271 EKLEFIDPDGTVALADMRKKSIMPALMYGDRDDNLFEHFSAVQLGVYTAKDYADI 330

Qy 301 LEFLVGRKVKDKLTGLSSEGOKAQDYVCRLPPRIRRLERAGRAKEAPTMPSWIFRQ 360
Db 331 LEFHGRNEVEKLTGSSGRRAQDYVCGLAPRKLEERAQAKHAKSVPSWIFRQE 390

Qy 361 VKL 363
Db 391 IKL 393

RESULT 14
T07653
acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) precursor - potato
Db 211 TENNPHLGFIYTYSQERATFISHGNTARHAKHGDIMKLAQVGTTIAADEKRHETAYTKIV 270
Qy 241 EKLEFIDPDGTVALAFADMRKKSIMPALMYGDRDDNLFDHFSAVQLGVYTAKDYADI 300
Db 271 EKLEFIDPDGTVALADMRKKSIMPALMYGDRDDNLFEHFSAVQLGVYTAKDYADI 330

Qy 301 LEFLVGRKVKDKLTGLSSEGOKAQDYVCRLPPRIRRLERAGRAKEAPTMPSWIFRQ 360
Db 331 LEFHGRNEVEKLTGSSGRRAQDYVCGLAPRKLEERAQAKHAKSVPSWIFRQE 390

Qy 361 VKL 363
Db 391 IKL 393

RESULT 14
T07653
acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) precursor - potato
Db 211 TENNPHLGFIYTYSQERATFISHGNTARHAKHGDIMKLAQVGTTIAADEKRHETAYTKIV 270
Qy 241 EKLEFIDPDGTVALAFADMRKKSIMPALMYGDRDDNLFDHFSAVQLGVYTAKDYADI 300
Db 271 EKLEFIDPDGTVALADMRKKSIMPALMYGDRDDNLFEHFSAVQLGVYTAKDYADI 330

Qy 301 LEFLVGRKVKDKLTGLSSEGOKAQDYVCRLPPRIRRLERAGRAKEAPTMPSWIFRQ 360
Db 331 LEFHGRNEVEKLTGSSGRRAQDYVCGLAPRKLEERAQAKHAKSVPSWIFRQE 390

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Accession: T07653
A;Molecule type: mRNA
A;Residues: 1-393 <TP>
A;Function: introduces a double bond at the delta(9) position of stearoyl-ACP gene
A;Pathway: fatty acid biosynthesis
C;Superfamily: acyl-[acyl-carrier-protein] desaturase
C;Keywords: fatty acid biosynthesis; oxidoreductase; unsaturated fatty acid biosynthe
F;1-65/Domain: signal sequence #status predicted <STG>
C;Accession: T10793
R;Liu, Q.; Singh, S.; Sharp, P.; Green, A.; Marshall, D.R.
Plant Physiol., 110, 1436, 1996
A;Title: Nucleotide sequence of a cDNA from *Gossypium hirsutum* encoding a stearoyl-ac
A;Reference number: 217148
A;Accession: T10793
A;Molecule type: mRNA
A;Residues: 1-397 <LIU>
A;Cross references: ENB: X5988; NID: 91217627
A;Experimental source: cultivar deltapine-16
C;Function:
A;Description: fatty acid biosynthesis
C;Superfamily: acyl-[acyl-carrier-protein] desaturase
C;Keywords: fatty acid biosynthesis; oxidoreductase; unsaturated fatty acid biosynthe
F;66-397/Product: acyl-[acyl-carrier protein] desaturase #status predicted <MAT>

Query Match 84.1%; Score 16105; DB 2; Length 397;
Best Local Similarity 84.0%; Pred. No. 7.3e-114;
Matches 305; Conservative 21; Mismatches 36; Indels 1; Gaps 1;

Qy 2 STLKSGSKVEVNLRKPFMPREHVQVTHSMPPQKIEFKSLDNWAEEENILVHLKPVEK 61
Db 35 STPGSGKEVGNLKKPPTPKEVQVTHSMPPKIEFKSLGNAAENILVHLKPVEK 94

Qy 62 WOPQDFLPDPASDGFDEQYRELRAKEIPDDYFVVLVGDMDTTEALPTYQTMNLTDG 121
Db 95 WOPQDFLPDPNSDGFDEQYRELRAKEIPDDYFVVLVGDMDTTEALSTQTMNLTDG 154

Qy 122 RDETGAQPTSWAIWTRATAEENRGDLNLKLYLSGRVDMRQIEKTQYLIGSGMDPRT 181
Db 155 RDETGAQPTSWAIWTRATAEENRGDLNLKLYLSGRVDMRQIEKTQYLIGSGMDPRT 214

Qy 182 ENSPYLGFIYTYSQERATFISHGNTARQAKHGDIKLAQICGTIAADEKRHETAYTKIV 241
Db 299; Conservative 34; Mismatches 30; Indels 0; Gaps 0;

Db	215	ENSPYRGFIYTFSQERATEFISHGNTRGLAKEYGDINLAQICGSIASDEKRHETAYTKIVE	274
Qy	242	KLFIEDDPGTVLAFADMMRKISMPAHMLMYGRDDNLFDIHSAYAQRIGVYTAQDYADIL	301
Db	275	KLFIEDDPDETLAFADMMKKIAMPAAEFIDGRDNLFDIHSAYAQRIGVYTAQYVDIV	334
Qy	302	EFLVGRWKVKDPLTGLSAEGGKAQDYVCRLUPPRIRLEERAQGRAK-EAPTMPEFSWTFDRC	360
Db	335	EHLVDRWKVKELAGLUSAEGRAQDYCSSLRSRIRLEERAQEKAOGSTPVSFSTWTFDRC	394
Qy	361	VKL 363	
Db	395	VKL 397	

Search completed: March 7, 2003, 03:10:30
Job time : 23 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 7, 2003, 03:10:02 : Search time 16 Seconds (without alignments)
956.736 Million cell updates/sec

Title: US-10-017-145-1
Perfect score: 1916
Sequence: ASTLKGSKKEVNLKKPFMP.....RAKEAPTMPSWIFDROVKL 363

Scoring table: BLOSUM62
Gapext 0.5

Searched: 188354 seqs, 42170167 residues

Total number of hits satisfying chosen parameters: 188354

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:
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 2: /cgn2_6/podata/1/pubpaas/US08_NEW_PUB.pep:
 3: /cgn2_6/podata/1/pubpaas/US06_NEW_PUB.pep:
 4: /cgn2_6/podata/1/pubpaas/US06_PUBCOMB.pep:
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 6: /cgn2_6/podata/1/pubpaas/US07_PUBCOMB.pep:
 7: /cgn2_6/podata/1/pubpaas/PCTRUS_PUBCOMB.pep:
 8: /cgn2_6/podata/1/pubpaas/TUBCOMB.pep:
 9: /cgn2_6/podata/1/pubpaas/US09_NEW_PUB.pep:
 10: /cgn2_6/podata/1/pubpaas/US09_PUBCOMB.pep:
 11: /cgn2_6/podata/1/pubpaas/US10_NEW_PUB.pep:
 12: /cgn2_6/podata/1/pubpaas/US10_PUBCOMB.pep:
 13: /cgn2_6/podata/1/pubpaas/US60_NEW_PUB.pep:
 14: /cgn2_6/podata/1/pubpaas/US60_PUBCOMB.pep:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1916	100.0	363	10 US-09-988-929A-1	Sequence 1, Appli
2	1916	100.0	363	12 US-10-017-445-1	Sequence 1, Appli
3	1637	85.4	396	10 US-09-837-751-2	Sequence 2, Appli
4	291	15.2	54	9 US-09-730-733-12	Sequence 12, Appli
5	286	14.9	54	9 US-09-730-763-16	Sequence 16, Appli
6	283	14.8	54	9 US-09-730-763-15	Sequence 13, Appli
7	276	14.4	54	9 US-09-730-763-18	Sequence 15, Appli
8	273	14.2	52	9 US-09-730-763-27	Sequence 27, Appli
9	273	14.2	52	9 US-09-730-763-31	Sequence 31, Appli
10	271	14.1	52	9 US-09-730-763-31	Sequence 17, Appli
11	271	14.1	54	9 US-09-730-763-17	Sequence 14, Appli
12	270	14.1	54	9 US-09-730-763-14	Sequence 4, Appli
13	267	13.9	338	9 US-09-730-763-4	Sequence 37, Appli
14	267	13.9	338	9 US-09-730-763-37	Sequence 28, Appli
15	262	13.7	52	9 US-09-730-763-28	Sequence 29, Appli
16	260	13.6	52	9 US-09-730-763-29	Sequence 33, Appli
17	254	13.3	54	9 US-09-730-763-33	Sequence 30, Appli
18	254	13.3	52	9 US-09-730-763-30	
19	247	12.9	52	9 US-09-730-763-34	

ALIGNMENTS

RESULT 1
US-09-988-929A-1
; Sequence 1, Application US/09888929A
; Patent No. US201020150982A1
; GENERAL INFORMATION:
; APPLICANT: Brookhaven Science Associates
; APPLICANT: Shanklin, John
; APPLICANT: Cahoon, Edgar B.
; TITLE OF INVENTION: Mutant Fatty Acid Desaturase
; FILE REFERENCE: BSA 02-01; CIP of 09/233,856, filed 01/19/99
; CURRENT APPLICATION NUMBER: US/09-988-929A
; CURRENT FILING DATE: 2001-11-19
; PRIORITY DATE: 1999-01-19
; PRIORITY NUMBER: 09/233,856
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 1
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Ricinus communis
US-09-988-929A-1

Query Match 100.0%; Score 1916; DB 10; Length 363;
Best Local Similarity 100.0%; Pred. No. 7.8e-169; Mismatches 0; Indels 0; Gaps 0;

1 ASTLKGSKKEVNLKKPFMPPREVHIVOTHSMPPQKEIEFKSLDNAAEENLVHLKPVK 60
Db 1 ASTLKGSKKEVNLKKPFMPPREVHIVOTHSMPPQKEIEFKSLDNAAEENLVHLKPVK 60
Qy 61 CWQPODFLPDASDGFDEQVRLERAKEIPDDYFVVLGDMITEALPTVQTMLNPLDG 120
Db 61 CWQPODFLPDASDGFDEQVRLERAKEIPDDYFVVLGDMITEALPTVQTMLNPLDG 120
Qy 121 VRDETAGSPTSWAIWTRAWTAENRHDLLNKYLQLSGRVDMRQIEXTIQYLIGSGMDPR 180
Db 121 VRDETAGSPTSWAIWTRAWTAENRHDLLNKYLQLSGRVDMRQIEXTIQYLIGSGMDPR 180
Qy 181 TENSPILGFIITSFORERATISHGNNTARQAEFHGDKLQAQCGTTIAADEKHEATAKIV 240
Db 181 TENSPILGFIITSFORERATISHGNNTARQAEFHGDKLQAQCGTTIAADEKHEATAKIV 240

Page 2

QY 241 EKLEIPDPGTVLAFADMRRKKISMPAHMLYGRDDNLDFHESAVAQLRGVYTAKDYADI 300
 Db 241 EKLEIPDPGTVLAFADMRRKKISMPAHMLYGRDDNLDFHESAVAQLRGVYTAKDYADI 300
 1
 QY 301 LEFLVGRWKVDKLTLGLSABEGQKAQDYVCRLLPPIRRLERAQGRAKEAPTMPSWIFDQ 360
 Db 301 LEFLVGRWKVDKLTLGLSABEGQKAQDYVCRLLPPIRRLERAQGRAKEAPTMPSWIFDQ 360
 QY 361 VKL 363
 Db 361 VKL 363

RESULT 2
 US-10-017-145-1
 Sequence 1, Application US/10017145
 Patent No. US20020151019A1
 GENERAL INFORMATION:
 APPLICANT: Brookhaven Science Associates
 TITLE OF INVENTION: Mutant Fatty Acid Desaturase and Methods for Directed Mutagenesis
 FILE REFERENCE: CIP of 09/328,550 filed June 9, 1999; which was a CIP of 09/233,856 filed January 19, 1999
 CURRENT APPLICATION NUMBER: US/10/017/145
 CURRENT FILING DATE: 2001-12-14
 PRIOR APPLICATION NUMBER: 09/328,550
 PRIOR FILING DATE: 1999-06-09
 NUMBER OF SEQ ID NOS: 13
 SOFTWARE: Patentin version 3.1
 SEQ ID NO 1
 LENGTH: 363
 TYPE: PRT
 ORGANISM: Ricinus communis
 FEATURE:
 NAME/KEY: misc_feature
 OTHER INFORMATION: r.cinus communis delta 9 18:0 Acyl ACP Desaturase
 US-10-017-145-1

Query Match 100.0% Score 1916; DB 12; Length 363;
 Best Local Similarity 100.0% Pred. No. 7.8e-169;
 Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASTLSSGSKEVENLKKPFMPPREVQVTHSMPPKIEFKSLDNWAENILVHLKPVEK 60
 Db 1 ASTLSSGSKEVENLKKPFMPPREVQVTHSMPPKIEFKSLDNWAENILVHLKPVEK 60
 QY 61 CWQPODPLPDAFDGDFEQVRELRAKEIPLPDYFVVLGDMITEBALPYQTMLNTLDG 120
 Db 61 CWQPODPLPDAFDGDFEQVRELRAKEIPLPDYFVVLGDMITEBALPYQTMLNTLDG 120
 QY 121 VDETGAASPWSWAIINTRAAENRHGDLNKLYLGSRVDMOTEKTIYLIGSGMDPR 180
 Db 121 VDETGAASPWSWAIINTRAAENRHGDLNKLYLGSRVDMOTEKTIYLIGSGMDPR 180

QY 181 TENSPLGFITYTSQERATEFISHGNTARQAKEHGDIKLAQICGTIAADEKRHETAYTKIV 240
 Db 181 TENSPLGFITYTSQERATEFISHGNTARQAKEHGDIKLAQICGTIAADEKRHETAYTKIV 240

QY 241 EKLFELDPGTVLAFADMRRKKISMPAHMLYGRDDNLDFHESAVAQLRGVYTAKDYADI 300
 Db 241 EKLFELDPGTVLAFADMRRKKISMPAHMLYGRDDNLDFHESAVAQLRGVYTAKDYADI 300
 QY 301 LEFLVGRWKVDKLTLGLSAGGQKAQDYVCRLLPPIRRLERAQGRAKEAPTMPSWIFDQ 360
 Db 301 LEFLVGRWKVDKLTLGLSAGGQKAQDYVCRLLPPIRRLERAQGRAKEAPTMPSWIFDQ 360

QY 361 VKL 363
 Db 361 VKL 363

; TITLE OF INVENTION: Method of Modifying the Content of Cottonseed Oil
 ; CURRENT APPLICATION NUMBER: US/09/937,751
 ; CURRENT FILING DATE: 2001-04-18
 ; PRIOR APPLICATION NUMBER: US 60/198,124
 ; PRIOR FILING DATE: 2000-04-18
 ; NUMBER OF SEQ ID NOS: 35
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 396
 ; TYPE: PRT
 ; ORGANISM: Gossypium sp.
 ; US-09-837-751-2

Query Match 85.4% Score 1637; DB 10; Length 396;
 Best Local Similarity 85.1% Pred. No. 4.8e-143;
 Matches 308; Conservative 22; Mismatches 32; Indels 0; Gaps 0;

Qy 2 STLSSGSKEVENLKKPFMPPREVQVTHSMPPKIEFKSLDNWAENILVHLKPVEK 61
 Db 35 STLSSGSKEVGNLKKPFPTPKEVQVTHSMPPKIEFKSLDNWAENILVHLKPVEK 94
 Qy 62 WQPODPLPDAFDGDFEQVRELRAKEIPLPDYFVVLGDMITEBALPYQTMLNTLDG 121
 Db 95 WQPODPLPDAFDGDFEQVRELRAKEIPLPDYFVVLGDMITEBALPYQTMLNTLDG 154
 Qy 122 RDETGASPTSWAIINTRAAENRHGDLNKLYLGSRVDMOTEKTIYLIGSGMDPR 181
 Db 155 RDETGASLPWAINTRAAENRHGDLNKLYLGSRVDMQERTIONLIGSGMDPHT 214
 Qy 182 ENSPYLGFITYTSQERATEFISHGNTARQAKEHGDIKLAQICGTIAADEKRHETAYTKIV 241
 Db 215 ENSPYRGFLYTSQERATEFISHGNTGRLAKKEYGDIINLAQCGSTAASDERHETAYTKIV 274
 Qy 242 KLFELDPGTVLAFADMRRKKISMPAHMLYGRDDNLDFHESAVAQLRGVYTAKDYADIL 301
 Db 275 KLFELDPGTVLAFADMRRKKISMPAHMLYGRDDNLDFHESAVAQLRGVYTAKDYADIV 334
 Qy 302 EFLYGRWKVDKLTLGLSAGGQKAQDYVCRLLPPIRRLERAQGRAKEAPTMPSWIFDQV 361
 Db 335 EHLVDRWKVKELAGLSAGGQKAQDYLCSLSPSRIRLERAQEKAAPSPVPSNIFDREV 394

RESULT 4
 US-09-730-763-12
 Sequence 12, Application US/09730763
 Publication No. US20020192781A1
 GENERAL INFORMATION:
 APPLICANT: JACKSON, Mary
 APPLICANT: GIQUEL, Brigitte
 APPLICANT: DUNNER, L.L.P.
 TITLE OF INVENTION: DESAUTURASE ANTIGEN OF MYCOBACTERIUM
 NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: C/O Finnegan Henderson, Farrabow, Garrett & Dunner, L.L.P.
 STREET: 1300 I Street, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

*RESULT 3
 US-09-751-2

```

; COMPUTER: IBM PC compatible
; SOFTWARE: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/730,763
;   FILING DATE:
;   CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 08/917,299
;       FILING DATE:
;         ATTORNEY/AGENT INFORMATION:
;           NAME: MEYERS, Kenneth J.
;           REGISTRATION NUMBER: 25,146
;           REFERENCE/DOCKET NUMBER: 03495.0156-00
;           TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202) 408-4400
;             TELEFAX: (202) 408-4400
;           INFORMATION FOR SEQ ID NO: 12:
;             SEQUENCE CHARACTERISTICS:
;               LENGTH: 54 amino acids
;               STRANDEDNESS: single
;               TOPOLOGY: linear
;               MOLECULE TYPE: peptide
;               US-09-730-763-12

Query Match      15.2%;  Score 291;  DB 9;  Length 54;
Best Local Similarity 100.0%;  Pred. No. 3.7e-20;
Matches 54;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
US-09-730-763-16

; SEQUENCE CHARACTERISTICS:
;   LENGTH: 54 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   US-09-730-763-16

RESULT 6
US-09-730-763-13
; Sequence 13, Application US/09730763
; Publication No. US20020192781A1
; GENERAL INFORMATION:
;   APPLICANT: JACKSON, Mary
;   APPLICANT: GIQUEL, Brigitte
;   TITLE OF INVENTION: DESATURASE ANTIGEN OF MYCOBACTERIUM
;   TITLE OF INVENTION: DESATURASE ANTIGEN OF TUBERCULOSIS
;   NUMBER OF SEQUENCES: 37
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: C/O Finnegan Henderson, Farrabow, Garrett &
;     STREET: 1300 I Street, N.W.
;     CITY: Washington
;     STATE: D.C.
;     COUNTRY: USA
;     ZIP: 20005
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/730,763
;     FILING DATE:
;     CLASSIFICATION:
;       PRIOR APPLICATION NUMBER: 08/917,299
;       FILING DATE:
;       ATTORNEY/AGENT INFORMATION:
;         NAME: MEYERS, Kenneth J.
;         REGISTRATION NUMBER: 25,146
;         TELECOMMUNICATION INFORMATION:
;           TELEPHONE: (202) 408-4400
;           TELEFAX: (202) 408-4400
;           INFORMATION FOR SEQ ID NO: 13:
;             SEQUENCE CHARACTERISTICS:
;               LENGTH: 54 amino acids
;               STRANDEDNESS: single
;               TOPOLOGY: linear
;               MOLECULE TYPE: peptide
;               US-09-730-763-13

Query Match      14.9%;  Score 286;  DB 9;  Length 54;
Best Local Similarity 98.1%;  Pred. No. 1.1e-19;
Matches 53;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;
US-09-730-763-16

; SEQUENCE CHARACTERISTICS:
;   LENGTH: 54 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   US-09-730-763-16

RESULT 7
US-09-730-763-14
; Sequence 14, Application US/09730763
; Publication No. US20020192781A1
; GENERAL INFORMATION:
;   APPLICANT: JACKSON, Mary
;   APPLICANT: GIQUEL, Brigitte
;   TITLE OF INVENTION: DESATURASE ANTIGEN OF MYCOBACTERIUM
;   TITLE OF INVENTION: DESATURASE ANTIGEN OF TUBERCULOSIS
;   NUMBER OF SEQUENCES: 37
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: C/O Finnegan Henderson, Farrabow, Garrett &
;     STREET: 1300 I Street, N.W.
;     CITY: Washington
;     STATE: D.C.
;     COUNTRY: USA
;     ZIP: 20005
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/730,763
;     FILING DATE:
;     CLASSIFICATION:
;       PRIOR APPLICATION NUMBER: 08/917,299
;       FILING DATE:
;       ATTORNEY/AGENT INFORMATION:
;         NAME: MEYERS, Kenneth J.
;         REGISTRATION NUMBER: 25,146
;         TELECOMMUNICATION INFORMATION:
;           TELEPHONE: (202) 408-4400
;           TELEFAX: (202) 408-4400
;           INFORMATION FOR SEQ ID NO: 16:
;             SEQUENCE CHARACTERISTICS:
;               LENGTH: 54 amino acids
;               STRANDEDNESS: single
;               TOPOLOGY: linear
;               MOLECULE TYPE: peptide
;               US-09-730-763-14

Query Match      14.9%;  Score 286;  DB 9;  Length 54;
Best Local Similarity 98.1%;  Pred. No. 1.1e-19;
Matches 53;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;
US-09-730-763-16

; SEQUENCE CHARACTERISTICS:
;   LENGTH: 54 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   US-09-730-763-16

RESULT 7

```

US-09-730-763-15
 ; Sequence 15; Application US/09730763
 ; Publication No. US20020192781A1
 ; GENERAL INFORMATION:
 ; APPLICANT: JACKSON, Mary
 ; ATTORNEY/AGENT INFORMATION:
 ; TITLE OF INVENTION: DESATURASE ANTIGEN OF MYCOBACTERIUM
 ; TITLE OF INVENTION: TUBERCULOSIS
 ; NUMBER OF SEQUENCES: 37
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: C/O Finnegan Henderson, Farrabow, Garrett &
 ; STREET: 1300 I Street, N.W.
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/730,763
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 08/917,299
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MEYERS, Kenneth J.
 ; REFERENCE/DOCKET NUMBER: 25,146
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 408-4400
 ; TELEFAX: (202) 408-4400
 ; INFORMATION FOR SEQ ID NO: 18:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 54 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-09-730-763-18

Query Match 14 4%; Score 276; DB 9; Length 54;
 Best Local Similarity 96.3%; Pred. No. 98-19; Gaps 0; Gaps 0;

Qy 98 LVGDMITEALPPTYQTMLNTLGVDRDGASPTSWAINTWATAEENRGDLLN 151
 Db 1 LVGDMITEALPPTYQTMLNTLGVDRDGASPTSWAINTWATAEENRGDLLN 54

RESULT 9
 US-09-730-763-27
 ; Sequence 27; Application US/09730763
 ; Publication No. US20020192781A1
 ; GENERAL INFORMATION:
 ; APPLICANT: JACKSON, Mary
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MEYERS, Kenneth J.
 ; REFERENCE/DOCKET NUMBER: 25,146
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 408-4400
 ; TELEFAX: (202) 408-4400
 ; INFORMATION FOR SEQ ID NO: 15:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 54 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-09-730-763-15

Query Match 14 8%; Score 283; DB 9; Length 54;
 Best Local Similarity 94.4%; Pred. No. 2e-19; Gaps 0; Gaps 0;

Qy 98 LVGDMITEALPPTYQTMLNTLGVDRDGASPTSWAINTWATAEENRGDLLN 151
 Db 1 LVGDMITEALPPTYQTMLNTLGVDRDGASPTSWAINTWATAEENRGDLLN 54

RESULT 8
 US-09-730-763-18
 ; Sequence 18; Application US/09730763
 ; Publication No. US20020192781A1
 ; GENERAL INFORMATION:
 ; APPLICANT: JACKSON, Mary
 ; ATTORNEY/AGENT INFORMATION:
 ; TITLE OF INVENTION: DESATURASE ANTIGEN OF MYCOBACTERIUM
 ; TITLE OF INVENTION: TUBERCULOSIS
 ; NUMBER OF SEQUENCES: 37
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: C/O Finnegan Henderson, Farrabow, Garrett &
 ; STREET: 1300 I Street, N.W.
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/730,763
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 08/917,299
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MEYERS, Kenneth J.
 ; REFERENCE/DOCKET NUMBER: 25,146
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 408-4400
 ; TELEFAX: (202) 408-4400

;

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 52 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-730-763-27

RESULT 11

Query Match 14.2%; Score 273; DB 9; Length 52;

Best Local Similarity 100.0%; Pred. No. 1.6e-18;

Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 186 YLGFIYTSFQERATFISHGNTARQAKEHGDIKLQAQICGTTAADEKRHETAYT 237

Db 1 YLGFIYTSFQERATFISHGNTARQAKEHGDIKLQAQICGTTAADEKRHETAYT 52

;

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: C/o Finneghan Henderson, Farrabow, Garrett &

APPLICANT: Dunner, L.L.P.

STREET: 1300 I Street, N.W.

CITY: Washington

STATE: D.C.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn ReLease #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/730,763

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/917,299

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: MEYERS, Kenneth J.

REGISTRATION NUMBER: 25,146

REFERENCE/DOCKET NUMBER: 03495.0156-00

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 408-4000

TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 54 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Peptide

US-09-730-763-17

RESULT 12

Query Match 14.1%; Score 271; DB 9; Length 54;

Best Local Similarity 98.1%; Pred. No. 2.5e-18;

Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 186 YLGFIYTSFQERATFISHGNTARQAKEHGDIKLQAQICGTTAADEKRHETAYT 237

Db 1 YLGFIYTSFQERATFISHGNTARQAKEHGDIKLQAQICGTTAADEKRHETAYT 52

;

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: C/o Finneghan Henderson, Farrabow, Garrett &

APPLICANT: Dunner, L.L.P.

STREET: 1300 I Street, N.W.

CITY: Washington

STATE: D.C.

ZIP: 20005

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/730,763
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/917,299
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: MEYERS, Kenneth J.
 REGISTRATION NUMBER: 03495.0156-00
 REFERENCE/DOCKET NUMBER: 03495.0156-00
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 408-4000
 TELEFAX: (202) 408-4400
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 54 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-730-763-14

Query Match Score 270; DB 9; Length 54;
 Best Local Similarity 92.6%; Pred. No. 3.e-18;
 Matches 50; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 98 LVGDMITEEALPYQTMLNTLDGVDRTEGASPTSWAIWTRAWTAEENRHGDLLN 151
 Db 1 LVGDMITEEALPYQTMLNTLDGVDRTEGASPTSWAIWTRAWTAEENRHGDLLH 54

RESULT 13
 US-09-730-763-4
 Sequence 4, Application US/09710763
 Publication No. US/0020192781A1
 GENERAL INFORMATION:
 APPLICANT: JACKSON, Mary
 APPLICANT: GIQUEL, Brigitte
 TITLE OF INVENTION: DESATURASE ANTIGEN OF MYCOBACTERIUM
 NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: C/o Finnegan Henderson, Farrabow, Garrett &
 STREET: 1300 I Street, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20005

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/730,763
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/917,299
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: MEYERS, Kenneth J.
 REFERENCE/DOCKET NUMBER: 03495.0156-00
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 408-4000

TELEFAX: (202) 408-4400
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 338 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-730-763-4

Query Match Score 267; DB 9; Length 338:
 Best Local Similarity 25.6%; Pred. No. 9.3e-17;
 Matches 84; Conservative 54; Mismatches 128; Indels 62; Gaps 11;

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 Db 1 MSALKLTQQLHELEP-----VVERLYNRLHLSMH----KPWNPHDYL---PWSDGKNY 46
 Qy 76 -----FDEQVRELRLRPAKEPDYFVVLGDMITEBALPYQ---TMLNLTDGVDRDET 125
 Db 47 Y ALGGQDDWPDSKLSDVAQ-----VAMYQNLVTDNLFSYHRETAMNGMDG---- 94
 Qy 126 GASPTSWAIWTRAWTAEENRHGDLLNLYLSGRVDMRQIETQVIGSGNDPRTENSP 185
 Db 95 -----ANGQWRWRWTABENRHTALRDYLVVRSVDEPELERLVRLEVNRGSPGQNHQ 149
 Qy 186 YL-----GFIYTSQEERATEISHGNATQRQAKEHGDIKLQAICGTTIADEKRHETAY'K 238
 Qy 150 HYFAESELSTDVSYVSQELATRISHRT---SKACNDPVAODLMKTSADENLHMFYRD 206
 Db 207 VSEAAFDLVPN-----OAMSLHLILSHFQMGPQFQYEFRRKAVVIAVGSVYDPRHL 259

RESULT 14
 US-09-730-763-37
 Sequence 37, Application US/09730763
 Publication No. US/0020192781A1
 GENERAL INFORMATION:
 APPLICANT: JACKSON, Mary
 APPLICANT: GIQUEL, Brigitte
 TITLE OF INVENTION: DESATURASE ANTIGEN OF MYCOBACTERIUM
 NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: C/o Finnegan Henderson, Farrabow, Garrett &
 STREET: 1300 I Street, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20005

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/730,763
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/917,299
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: MEYERS, Kenneth J.
 REFERENCE/DOCKET NUMBER: 03495.0156-00
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 408-4000

```

;
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 338 amino acids
; TYPE: amino acid
; TOPOLOGY: Linear
; MOLECULE TYPE: protein
; US-09-730-763-37

Query Match 13.9%; Score 267; DB 9; Length 338;
Best Local Similarity 25.6%; Pred. No. 9 3e-17;
Matches 84; Conservative 54; Mismatches 128; Indels 62; Gaps 11;
Query Match 13.7%; Score 262; DB 9; Length 52;
Best Local Similarity 96.2%; Pred. No. 1.7e-17;
Matches 50; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
SEQUENCE CHARACTERISTICS:
; LENGTH: 52 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-730-763-28

;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-730-763-28

;
; Search completed: March 7, 2003, 03:14:49
; Job time : 17 secs

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Db 1 MSAKLTDIQLLHEP-----VKEVLYNRLHSMH----KPDWPHDYI--PWSDGKNY 46
QY 76 -----PDEQVRELRERAKEIPDIDYFVVLVGDMITEALPYQ--TMLNLTDGVRDET 125
Db 47 YALGGQWDQDPSKLSDVQA-----VAMVNQULVTEONLPSPYHETIAMNMGMGDG--- 94
QY 126 GASPTSWAIWTRAWTAEENRHGDLLNLYLSGRGMQRIEKTQYLIGSGMMPRTENSP 185
Db 95 -----AWGQWNWRWTAEENRHGDLLNLYLSGRGMQRIEKTQYLIGSGMMPRTENSP 149
QY 186 YL-----GFIYTSFQERATFISHGNTRAQAEKGDIKLAQICGTIAADEKRHETAYTK 238
Db 150 HYFAESLTDSVLYVSFQELATRSHRN--GRACNDPVADQLMAKISDENLHMIFYRD 206
Qy 239 IVERKLFDLDPDGTVLAFADMMRKISMPAHMLYDGRDNLFDESAVQRLGYYTAKRYA 298
Db 207 VSEAAFDLVNP-----QAMKSLHLILSHFQMPGFQVPEFRRKAVVIAVGGVYDPRIHL 259
Qy 299 D-TLEFLYGRWKVDKLTLGSAEGQKAQD 325
Db 260 DEVVMPVLUKKWCIFEREDFTGECAKLRD 287

RESULT 15
US-09-730-763-28
Sequence 28 Application US/09730763
Publication No. US20020192781A1
GENERAL INFORMATION:
APPLICANT: JACKSON, Mary
APPLICANT: GIQUEL, Brigitte
TITLE OF INVENTION: DESATURASE ANTIGEN OF MYCOBACTERIUM
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: C/o Finnegan Henderson, Farrabow, Garrett &
STREET: 1300 I Street, N.W.
STATE: D.C.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.3.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/730-763
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/917,299
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MEYERS, Kenneth J.
REFERENCE DOCKET NUMBER: 03495-0156-00

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 7, 2003, 03:07:57 ; Search time 19 Seconds

(without alignments)
562.133 Million cell updates/sec

Title: US-10-017-145-1

Perfect score: 1916

Sequence: ASTLKGSKKEVENLKKPFMP.....RAKEAPTMFSWIFDRQVKL 363

Scoring table: BLOSUM62

Gapext 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA: *

- 1: /cgn2_6/pctodata/2/iaa/5A_COMB.pep:*
- 2: /cgn2_6/pctodata/2/iaa/5B_COMB.pep:*
- 3: /cgn2_6/pctodata/2/iaa/6A_COMB.pep:*
- 4: /cgn2_6/pctodata/2/iaa/6B_COMB.pep:*
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- 6: /cgn2_6/pctodata/2/iaa/backtose1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	1916	100.0	396	1	US-08-519-798-3		Sequence 3, Appl1
2	1916	100.0	396	1	US-08-520-560-		Sequence 3, Appl1
3	1916	100.0	396	1	US-08-471-791-16		Sequence 4, Appl1
4	1916	100.0	396	4	US-08-926-522-4		Sequence 16, Appl1
5	1916	100.0	396	5	PCT-US91-01746-16		Sequence 6, Appl1
6	1753	91.5	391	1	US-07-993-657-6		Sequence 6, Appl1
7	1753	91.5	391	1	US-08-471-587-6		Sequence 6, Appl1
8	1752	91.4	396	1	US-08-471-791-13		Sequence 13, Appl1
9	1752	91.4	396	4	US-08-926-522-2		Sequence 13, Appl1
10	1752	91.4	396	5	PCT-US91-01746-13		Sequence 20, Appl1
11	1698	88.6	398	1	US-08-471-791-20		Sequence 6, Appl1
12	1698	88.6	398	4	US-08-926-522-6		Sequence 20, Appl1
13	1316	88.6	398	5	PCT-US91-01746-20		Sequence 4, Appl1
14	1316	68.7	385	1	US-08-539-798-4		Sequence 4, Appl1
15	1316	68.7	385	1	US-08-329-560-4		Sequence 2, Appl1
16	1261	65.8	387	1	US-08-539-798-2		Sequence 2, Appl1
17	1261	65.8	387	1	US-08-329-560-2		Sequence 2, Appl1
18	1218	63.6	368	2	US-08-867-137-2		Sequence 12, Appl1
19	291	15.2	54	3	US-08-917-299-12		Sequence 16, Appl1
20	291	15.2	54	4	US-09-422-662-16		Sequence 13, Appl1
21	291	15.2	54	4	US-09-422-662-12		Sequence 16, Appl1
22	286	14.9	54	3	US-08-917-299-13		Sequence 13, Appl1
23	286	14.9	54	4	US-09-422-662-13		Sequence 15, Appl1
24	286	14.9	54	4	US-08-917-299-15		Sequence 15, Appl1
25	283	14.8	54	4	US-09-422-662-15		Sequence 18, Appl1
26	283	14.8	54	3	US-08-917-299-18		Sequence 17, Appl1
27	276	14.4	54	4	US-09-422-662-18		Sequence 14, Appl1
28	276	14.4	52	3	US-08-917-299-27		Sequence 17, Appl1
29	273	14.2	52	4	US-09-422-662-27		Sequence 14, Appl1
30	273	14.2	56	1	US-08-471-791-2		Sequence 14, Appl1
31	273	14.2	56	5	PCT-US91-01746-2		Sequence 14, Appl1
32	273	14.1	52	3	US-08-917-299-31		Sequence 14, Appl1
33	271	14.1	52	4	US-09-422-662-31		Sequence 14, Appl1
34	271	14.1	54	3	US-08-917-299-17		Sequence 14, Appl1
35	271	14.1	54	4	US-09-422-662-17		Sequence 14, Appl1
36	270	14.1	54	3	US-08-917-299-14		Sequence 14, Appl1
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38	270	14.1	57	1	US-08-471-791-7		Sequence 14, Appl1
39	267	13.9	57	5	PCT-US91-01746-7		Sequence 14, Appl1
40	267	13.9	338	3	US-08-917-299-4		Sequence 14, Appl1
41	267	13.9	338	4	US-09-422-662-4		Sequence 14, Appl1
42	267	13.9	338	4	US-09-422-662-37		Sequence 14, Appl1
43	267	13.9	52	3	US-08-917-299-28		Sequence 14, Appl1

ALIGNMENTS

RESULT 1
US-08-539-798-3
; Sequence 3, Application US/08539798
; Patent No. 5614400
; GENERAL INFORMATION:
; APPLICANT: CAHOON, Edgar B.
; TITLE OF INVENTION: Methods and Compositions Relating to Plant 6-Delta Palmitoyl-Acyl Carrier Protein Desaturase
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pioneer Hi-Bred International, Inc.
; STREET: 700 Capital Square, 400 Locust Street
; CITY: Des Moines
; STATE: Iowa
; ZIP: 50309
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/539,798
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION NUMBER: US 08/329,560
; APPLICATION NUMBER: US 08/329,560
; FILING DATE: 26-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Yales, Michael E.
; REGISTRATION NUMBER: 36,063
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (515) 248-4800
; TELEFAX: (515) 248-4844
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 396 amino acids
; REGISTRATION NUMBER: 0284US
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-539-798-3

Query Match 100.0%; Score 1916;
Best Local Similarity 100.0%; Pred. No. 2.2e-180;
Matches 363; Conservative 0; Mismatches 0; Gaps 0;
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Db 34 ASTLKGSKSEVENLKKPFMPPREVHQVTHSMPQKIEFKSLDNWAEENILVHLKPEVK 93
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 Db 94 CNOQDFLPDPASDGFDEVRLRERAKEIIPDDYFVVLYGDMITEEALPYYCTMLNTLDG 1.53
 Qy 121 VROETGASPTSWAINTRWTAAEENRHGDLLNKYLIGSGMDPR 1.80
 Db 154 VROETGASPTSWAINTRWTAAEENRHGDLLNKYLIGSGMDPR 2.13
 Qy 181 TENSPLYGFIYTSQERATFISHGNTARQAKEHGDIKLAQICGTTIAADEKRHETAYTKIV 2.40
 Db 214 TENSPLYGFIYTSQERATFISHGNTARQAKEHGDIKLAQICGTTIAADEKRHETAYTKIV 2.73
 Qy 241 EKLFEIDPDGTVLAFADMNRKKTISMPAHLMYGRDDNLFDHFSAVAORLGVTAKDYADI 3.00
 Db 274 EKLFEIDPDGTVLAFADMNRKKTISMPAHLMYGRDDNLFDHFSAVAORLGVTAKDYADI 3.33
 Qy 301 LEFLVGRHKVKDUTGLSAEGQKAQDYVCRLLPPIRRLERAQGRAKEAPTMPFSWIFDRO 3.60
 Db 334 LEFLVGRHKVKDUTGLSAEGQKAQDYVCRLLPPIRRLERAQGRAKEAPTMPFSWIFDRO 3.93
 Qy 361 VKL 363
 Db 394 VKL 396

RESULT 2
 US-08-329-560-3
 ; Sequence 3, Application US/08329560
 ; Patent No. 5654402
 ; GENERAL INFORMATION:
 ; APPLICANT: CAHOON, Edgar B.
 ; ATTORNEY/AGENT INFORMATION:
 ; APPLICANT: OHLROBEE, John B.
 ; TITLE OF INVENTION: Methods and Compositions Relating to
 ; Plant 6-Delta Paimitoyl-Acyl Carrier Protein Desaturase
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pioneer Hi-Bred International, Inc.
 ; STREET: 700 Capital Square, 400 Locust Street
 ; CITY: Des Moines
 ; STATE: Iowa
 ; ZIP: 50309
 ; COUNTRY: US
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC DOS/MS-DOS
 ; SOFTWARE: Patents Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/329,560
 ; FILING DATE: 26-OCT-1994
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Yates, Michael E.
 ; REGISTRATION NUMBER: 36,063
 ; REFERENCE/DOCKET NUMBER: 0284US
 ; TELEPHONE: (515) 248-4800
 ; TELEFAX: (515) 248-4844
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 396 amino acids
 ; STRANDDNESS:
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; US-08-329-560-3

Query Match 100.0% Score 1916; DB 1; Length 396;
 Best Local Similarity 100.0% Pre: No. 2.; e-NO: 3;
 Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 34 ASTLKGSKSEVENLKKPFMPPREVHQVTHSMPQKIEFKSLDNWAEENILVHLKPEVK 93
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 Db 94 CNOQDFLPDPASDGFDEVRLRERAKEIIPDDYFVVLYGDMITEEALPYYCTMLNTLDG 1.53
 Qy 121 VROETGASPTSWAINTRWTAAEENRHGDLLNKYLIGSGMDPR 1.80
 Db 154 VROETGASPTSWAINTRWTAAEENRHGDLLNKYLIGSGMDPR 2.13
 Qy 181 TENSPLYGFIYTSQERATFISHGNTARQAKEHGDIKLAQICGTTIAADEKRHETAYTKIV 2.40
 Db 214 TENSPLYGFIYTSQERATFISHGNTARQAKEHGDIKLAQICGTTIAADEKRHETAYTKIV 2.73
 Qy 241 EKLFEIDPDGTVLAFADMNRKKTISMPAHLMYGRDDNLFDHFSAVAORLGVTAKDYADI 3.00
 Db 274 EKLFEIDPDGTVLAFADMNRKKTISMPAHLMYGRDDNLFDHFSAVAORLGVTAKDYADI 3.33
 Qy 301 LEFLVGRHKVKDUTGLSAEGQKAQDYVCRLLPPIRRLERAQGRAKEAPTMPFSWIFDRO 3.60
 Db 334 LEFLVGRHKVKDUTGLSAEGQKAQDYVCRLLPPIRRLERAQGRAKEAPTMPFSWIFDRO 3.93
 Qy 361 VKL 363
 Db 394 VKL 396

RESULT 3
 US-08-471-791-16
 ; Sequence 16, Application US/08471791
 ; Patent No. 5723395
 ; GENERAL INFORMATION:
 ; APPLICANT: Thompson, Gregory A.
 ; ATTORNEY/AGENT INFORMATION:
 ; APPLICANT: Knuf, Vic C.
 ; TITLE OF INVENTION: Plant Desaturases -Compositions
 ; NUMBER OF SEQUENCES: 45
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Calgene, Inc.
 ; STREET: 1920 15th Street
 ; CITY: Davis
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 95616
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB storage
 ; COMPUTER: Apple Macintosh
 ; OPERATING SYSTEM: Macintosh 7.1
 ; SOFTWARE: MicrosoftWord 5.1 (a)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/471,791
 ; FILING DATE: 6-JUNE-95
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/762,762
 ; FILING DATE: 16-SEP-1991
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US91/01746
 ; FILING DATE: 14-MAR-1991
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/615,784
 ; FILING DATE: 14-NOV-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/567,373
 ; FILING DATE: 13-AUG-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/494,106
 ; FILING DATE: 16-MAR-1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lassen, Elizabeth

REGISTRATION NUMBER: 31,845
 NAME: Donna E. Scherer
 REGISTRATION NUMBER: 34,719
 NAME: Carl J. Schwedler
 REGISTRATION NUMBER: 36,924
 REFERENCE/DOCKET NUMBER: CGNE 69-5
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (916) 753-6313
 TELEX: 350370 CGNE
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 396 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-471-791-16

Query Match 100.0%; Score 1916; DB 1; Length 396;
 Best Local Similarity 100.0%; Pred. No. 2.2e-180;
 Matches 363; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 ASTLKGSKKEVENLKKPMPREHYQVTHSMPKQIEFKSLDNAAEENILVHLKPVEK
 Db 34 ASTLKGSKKEVENLKKPMPREHYQVTHSMPKQIEFKSLDNAAEENILVHLKPVEK 93

Qy 61 CWPQDPFLPDPAASDGFDEVRLERAKEIIDDYFVVLVGDMITEALPYQTOMLNTLDG 120
 Db 94 CWPQDPFLPDPAASDGFDEVRLERAKEIIDDYFVVLVGDMITEALPYQTOMLNTLDG 153

Qy 121 VRDETAGSPTSWAIWTRATAEENRGDLANKYLGSRYDMRQEKTQIQLIGSGMDPR 180
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Qy 301 LEFLVGRWKVDKLGLSAEGOKAODYVCRLPPIRRIEERAGRAKEAPTMPSWIFDRO 360
 Db 334 LEFLVGRWKVDKLGLSAEGOKAODYVCRLPPIRRIEERAGRAKEAPTMPSWIFDRO 393

RESULT 4
 US-08-471-791-16

Sequence 4, Application US/08926522
 Patent No. 6426447
 CORRESPONDENCE ADDRESS: 23
 APPLICANT: Vic C. Knauf
 TITLE OF INVENTION: PLANT SEED OILS
 NUMBER OF SEQUENCES: 23
 ADDRESSSEE: Calgene, Inc.
 CITY: Davis
 STATE: CA
 COUNTRY: USA
 ZIP: 95616

COMPATIBLE READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Macintosh 7.1
 SOFTWARE: Microsoft Word 5.1(a)
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/926,522
 FILING DATE:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/458,173
 FILING DATE: 2-June-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Elizabeth Lassen
 REGISTRATION NUMBER: 31,845
 NAME: Donna E. Scherer
 REGISTRATION NUMBER: 34,719
 NAME: Carl J. Schwedler
 REGISTRATION NUMBER: 36,924
 REFERENCE/DOCKET NUMBER: CGNE DES
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (916) 753-6313
 TELEFAX: (916) 753-1510
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 396 amino acids
 TYPE: amino acid
 MOLECULE TYPE: protein

Query Match 100.0%; Score 1916; DB 4; Length 396;
 Best Local Similarity 100.0%; Pred. No. 2.2e-180;
 Matches 363; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 ASTLKGSKKEVENLKKPMPREHYQVTHSMPKQIEFKSLDNAAEENILVHLKPVEK 60
 Db 34 ASTLKGSKKEVENLKKPMPREHYQVTHSMPKQIEFKSLDNAAEENILVHLKPVEK 93

Qy 61 CWPQDPFLPDPAASDGFDEVRLERAKEIIDDYFVVLVGDMITEALPYQTOMLNTLDG 120
 Db 94 CWPQDPFLPDPAASDGFDEVRLERAKEIIDDYFVVLVGDMITEALPYQTOMLNTLDG 153

Qy 121 VRDETAGSPTSWAIWTRATAEENRGDLANKYLGSRYDMRQEKTQIQLIGSGMDPR 180
 Db 154 VRDETAGSPTSWAIWTRATAEENRGDLANKYLGSRYDMRQEKTQIQLIGSGMDPR 213

Qy 181 TNSPYLGFIITSFQERATEFISHGNTARQAOKEHGDIKLAICGTTIAADEKRHETAYTKIV 240
 Db 214 TNSPYLGFIITSFQERATEFISHGNTARQAOKEHGDIKLAICGTTIAADEKRHETAYTKIV 273

Qy 241 EKLFIEDPDPGTWLAFAADMRRKKSIMPAHLYMDGRDNLFDHSAVAQRQGYYTAKYADI 300
 Db 274 EKLFIEDPDPGTWLAFAADMRRKKSIMPAHLYMDGRDNLFDHSAVAQRQGYYTAKYADI 333

Qy 301 LEFLVGRWKVDKLGLSAEGOKAODYVCRLPPIRRIEERAGRAKEAPTMPSWIFDRO 360
 Db 334 LEFLVGRWKVDKLGLSAEGOKAODYVCRLPPIRRIEERAGRAKEAPTMPSWIFDRO 393

RESULT 5
 PCT-US91-01746-16
 Sequence 16, Application PC/TUS9101746
 GENERAL INFORMATION:
 APPLICANT: Thompson, Gregory A.
 TITLE OF INVENTION: Plant Desaturases-Compositions and Uses
 NUMBER OF SEQUENCES: 43
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Calgene, Inc.
 STREET: 1920 Fifth Street
 CITY: Davis
 STATE: CA
 COUNTRY: USA
 ZIP: 95616

COMPATIBLE READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Macintosh 7.1
 SOFTWARE: Microsoft Word 5.1(a)
 CURRENT APPLICATION DATA:

COMPUTER READABLE FORM:
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Macintosh 6.0.7
 SOFTWARE: MicrosoftWord 4.0
 APPLICATION NUMBER: PCT/US91/01746
 FILING DATE: 19910314
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/615,784
 FILING DATE: 14 NOV-1990
 APPLICATION NUMBER: 07/567,373
 FILING DATE: 13-AUG-1990
 APPLICATION NUMBER: 07/494,106
 FILING DATE: 16 MAR-1990
 NAME: Lassen, Elizabeth
 REGISTRATION NUMBER: 31,845
 NAME: Donna E. Scherer
 REGISTRATION NUMBER: 34,719
 REFERENCE/DOCKET NUMBER: CGNE 69-3 WO
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (916) 753-6313
 TELEFAX: (916) 753-1510
 TELEX: 250370 CGNE
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 396 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US91-01746-16

Query Match 100.0% Score 1916; DB 5; Length 396;
 Best Local Similarity 100.0% Pred. No. 2_2e-180;
 Matches 363; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 ASTLKGSKKEVENLKKPMPREPVHQVTHSMPPQKIEFKSLDNWAENILVHLKPEK 60
 Db 34 ASTLKGSKKEVENLKKPMPREPVHQVTHSMPPQKIEFKSLDNWAENILVHLKPEK 93
 Qy 61 CWQPODFLPASDGFDEQVRERAKEIPDDYFVVLGDMITEALPTYQTMNLTDG 120
 Db 94 CWQPODFLPASDGFDEQVRERAKEIPDDYFVVLGDMITEALPTYQTMNLTDG 153
 Qy 121 VRDETGASPTSWATWTRANTAEENRHGDLINNKYLISGRVDMRQEKTQYLIGSGMDPR 180
 Db 154 VRDETGASPTSWATWTRANTAEENRHGDLINNKYLISGRVDMRQEKTQYLIGSGMDPR 213
 Qy 181 TENSPLYGLFTTSFOERATFISHNTARQAEKGDIKLAQICGTIAADEKRHETAYTKIV 240
 Db 214 TENSPLYGLFTTSFOERATFISHNTARQAEKGDIKLAQICGTIAADEKRHETAYTKIV 273
 Qy 241 EKLEFDIDPGTVLAFADMRRKKTISMPAHMLYDGDDNLFDHSAVAQRQGRAKEAFTMPFSWIFDRQ 300
 Db 274 EKLEFDIDPGTVLAFADMRRKKTISMPAHMLYDGDDNLFDHSAVAQRQGRAKEAFTMPFSWIFDRQ 333
 Qy 301 LEFLVGRWKVDKLTLGSAEQKAODYVCRLPPRIRLLEERAQGRAKEAFTMPFSWIFDRQ 360
 Db 334 LEFLVGRWKVDKLTLGSAEQKAODYVCRLPPRIRLLEERAQGRAKEAFTMPFSWIFDRQ 393
 Qy 361 VKL 363
 Db 394 VKL 396

APPLICANT: Yadav, Narendra S.
 APPLICANT: Perez, Grau Luis
 TITLE OF INVENTION: Nucleotide Sequence of Soybean Stearyl-ACP Desaturase cDNA
 NUMBER OF SEQUENCES: 7
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: E. I. du Pont de Nemours and Company
 STREET: 1007 Market Street
 CITY: Wilmington
 STATE: Delaware
 COUNTRY: U.S.A.
 ZIP: 19898
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
 COMPUTER: Macintosh System, 6.0
 OPERATING SYSTEM: Macintosh System, 6.0
 SOFTWARE: Microsoft Word, 4.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/995,657
 FILING DATE: 19921211
 FILING DATE: C) CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: GEIGER, KATHLEEN W.
 REGISTRATION NUMBER: 35,880
 REFERENCE/DOCKET NUMBER: BB_1022-B
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 302-892-8112
 TELEFAX: 302-892-7949
 TELEX: 835420
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 391 amino acids
 TYPE: AMINO ACID
 STRANDEDNESS: unknown
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-07-995-657-6

Query Match 91.5% Score 1753; DB 1; Length 391;
 Best Local Similarity 89.8%; Pred. No. 2_4e-164;
 Matches 326; Conservative 24; Mismatches 13; Indels 0; Gaps 0;

Qy 1 ASTLKGSKKEVENLKKPMPREPVHQVTHSMPPQKIEFKSLDNWAENILVHLKPEK 60
 Db 29 ASTLKGSKKEVENLKKPMPREPVHQVTHSMPPQKIEFKSLDNWAENILVHLKPEK 88
 Qy 61 CWQPODFLPASDGFDEQVRERAKEIPDDYFVVLGDMITEALPTYQTMNLTDG 120
 Db 89 CWQPODFLPASDGFDEQVRERAKEIPDDYFVVLGDMITEALPTYQTMNLTDG 148
 Qy 121 VRDETGASPTSWATWTRANTAEENRHGDLINNKYLISGRVDMRQEKTQYLIGSGMDPR 180
 Db 149 VRDETGASPTSWATWTRANTAEENRHGDLINNKYLISGRVDMRQEKTQYLIGSGMDPR 208
 Qy 181 TENSPLYGLFTTSFOERATFISHNTARQAEKGDIKLAQICGTIAADEKRHETAYTKIV 240
 Db 269 EKLEFDIDPGTVLAFADMRRKKTISMPAHMLYDGDDNLFDHSAVAQRQGRAKEAFTMPFSWIFDRQ 360
 Qy 301 LEFLVGRWKVDKLTLGSAEQKAODYVCRLPPRIRLLEERAQGRAKEAFTMPFSWIFDRQ 393
 Db 329 LEFLVGRWKVEQTGLSGESGRKAQEYVCGLPPRIRLLEERAQGRAKEAFTMPFSWIFDRQ 388
 Qy 361 VKL 363

RESULT 6
 US-07-995-657-6
 Sequence 6, Application US/07995657
 Patent No. 5443974
 GENERAL INFORMATION:
 APPLICANT: Hitz, William D.

RESULT 7

US-08-474-587-6 Sequence 6, Application US/08474587
Patent No. 5760206

GENERAL INFORMATION:

APPLICANT: Hitz, William D.
APPLICANT: Yadav, Narendra S.
APPLICANT: Perez-Grau, Luis

TITLE OF INVENTION: Nucleotide Sequence of Soybean Stearyl-ACP Desaturase cDNA

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS: E. I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: U.S.A.

ZIP: 19898

COMPUTER READABLE FORM:

OPERATING SYSTEM: Macintosh System, 6.0
SOFTWARE: Microsoft Word, 4.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/474,587
FILED DATE: 08-07-2006
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 95616
FILED DATE: 07-07-1991
ATTORNEY/AGENT INFORMATION:
NAME: Siegell, Barbara C.
REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: BB_1022-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4931
TELEFAX: 302-773-0164
TELEX: 835420

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: protein

Query Match 91.5%; Score 1753; DB 1; Length 391;
Best Local Similarity 89.8%; Pred. No. 2, 4e-164;
Matches 326; Conservative 24; Mismatches 13; Indels 0; Gaps 0;

Qy 1 ASTLRSSEKEYENLKPMPPEVHQVTHMPPQKETEISLDNPAEENLVHKPVEK 60
Db 29 ASTLRSSEKEYENIKKPPTPPREVHQVTHMAPPQKIEFKSLEDWADQNLTTHLPVEK 88

Qy 61 CWQPODFLPASDGFDQEVRERERAKEIIPDDYFVVLVGDMITEALPTYQTMLNLDG 120
Db 89 CWQPODFLPDPSSDGFPEQVKELRERAKEIIPDDYFVVLVGDMITEALPTYQTMLNLDG 148

Qy 121 VRDETAGSPTSAIWPTAWTAEENRHGDLLNKYLUSGRVDMRQIETKIQYLIGSGMDPR 180
Db 149 VRDETAGSLSAISWIATWTAEENRHGDLLNKYLUSGRVDMQKIEKTIQYLIGSGMDPR 208

Qy 181 TENSPLYLGFIITSFQERATFISHGNTARQAEHGDKLAQICGTIAADEKRHETAYTKIV 240
Db 209 TENSPLYLGFIITSFQERATFISHGNTARLAKEBHDIKLAQICGMIASDEKRHETAYTKIV 268

Qy 241 EKLFEIDDPGTVLAFADMMRKKISMPAHLMYGRDDNLFDHESAVAOQLGVYTAKYADI 300
Db 269 EKLFEIDDPGTVMAFADMMRKKIAMPAHLMYGRDNLEFDHESAVAOQLGVYTAKYADI 328

Qy 301 LEFLVGRWKVDKLTGESAEGQKAQDYVCRLLPRTRIRERAGRAEKTAMPFESWFDRQ 360
Db 329 LEFLVGRWKVEQLTGSSEGGRKAQEVYCLGLPRTTRLEERAQRGESSTLKFSWHDR 388

Qy 361 VKL 363
Db 389 VLL 391

RESULT 8
US-08-471-791-13
Sequence 13, Application US/08471791
Patent No. 572595

GENERAL INFORMATION:

APPLICANT: Thompson, Gregory A.
APPLICANT: Knauf, Vic C

TITLE OF INVENTION: Plant Desaturases-Compositions and Uses

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: California
COUNTRY: USA
ZIP: 95616

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1 (a)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/471,791
FILED DATE: 6-JUNE-95
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/01746
FILED DATE: 07/07/92, 762
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/471,791
FILED DATE: 16-SEP-1991
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 95616
FILED DATE: 14-NOV-1990
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/567,373
FILED DATE: 13-AUG-1990
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/494,106
FILED DATE: 16-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Lassen, Elizabeth
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CGNE 69-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
TELELEX: 350370 CGNE
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 396 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
 US-08-471-791-13

Query Match 91.4%; Score 1752; DB 1; Length 396;
 Best Local Similarity 90.1%; Pred. No. 3e-164;
 Matches 327; Conservative 18; Mismatches 18; Indels 0; Gaps 0;

QY 1 ASTLTKSGSKEVENLKKPFMPREHYVOTHSMPPQKIEFKSLDNAAEENLVLHKPVEK 60
 Db 34 ASTGSSSPPKVDNAKKPQQPREHVOTHSMPPQKEIFKSTEGWAEQNLLVHLHKPVEK 93

QY 61 CWAQDPLPDPASEGDEQVKELRAREKIPDDYFVVLGDMITEALPTYCTMLNTLDG 120
 Db 94 CWAQDPLPDPASEGDEQVKELRAREKIPDDYFVVLGDMITEALPTYCTMLNTLDG 153

QY 121 VRDETGAAPTWSAINTRWTAEENRHGDLLNKYLISGRVDRQIETKTQYLIGSGMDPR 180
 Db 154 VRDETGAAPTWSAINTRWTAEENRHGDLLNKYLISGRVDRQIETKTQYLIGSGMDPR 213

QY 181 TENSPLYGLFIYTSPQERATFISHGNTARQAKHDKLAQIGTIAADEKRHETATKIV 240
 Db 214 TENSPLYGLFIYTSPQERATFISHGNTARQAKHDKLAQIGTIAADEKRHETATKIV 273

QY 241 EKLFELIDPDGTVLAFADMRRKIKISMPAHLYMDGRDDNLFDHFSAVAORLGVTAKDYADI 300
 Db 274 EKLFELIDPDGTVLAFADMRRKIKISMPAHLYMDGRDDNLFEHFSAVAORLGVTAKDYADI 333

QY 301 LEFLVGRWKVDKTKTGLSAEGQRQDYYCRLPPRIRRLBERAGRAKADAPTMSFWSDRQ 360
 Db 334 LEFLVGRWKVADLTGLSGEGRKAQDYYCGLPPRIRRLBERAGRAKEGPVVDFSWIDRQ 393

QY 361 VKL 363
 Db 394 VKL 396

RESULT 9
 US-08-926-522-2
 Sequence 2, Application US/08926522
 PATENT NO. 6426447

GENERAL INFORMATION:
 APPLICANT: Gregory A. Thompson
 TITLE OF INVENTION: PLANT SEED OILS
 NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Calgene, Inc.
 STREET: 1920 Fifth Street
 CITY: Davis
 STATE: CA
 COUNTRY: USA
 ZIP: 95616

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Macintosh 7.1
 SOFTWARE: Microsoft Word 5.1(a)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/926,522
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/458,173
 FILING DATE: 2-June-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Elizabeth Lassen
 REGISTRATION NUMBER: 31,845
 NAME: Donna E. Scherer
 REGISTRATION NUMBER: 34,719
 NAME: Carl J. Schwieder
 REGISTRATION NUMBER: 36,924
 REFERENCE/DOCKET NUMBER: CGNE DES
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (916) 753-6313
 TELEFAX: (916) 753-1510
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 396 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-926-522-2

Query Match 91.4%; Score 1752; DB 4; Length 396;
 Best Local Similarity 90.1%; Pred. No. 3e-164;
 Matches 327; Conservative 18; Mismatches 18; Indels 0; Gaps 0;

QY 1 ASTLTKSGSKEVENLKKPFMPREHYVOTHSMPPQKIEFKSLDNAAEENLVLHKPVEK 60
 Db 34 ASTLGSSTPKVDNAKKPQQPREHVOTHSMPPQKEIFKSTEGWAEQNLLVHLHKPVEK 93

QY 61 CWAQDPLPDPASEGDEQVKELRAREKIPDDYFVVLGDMITEALPTYCTMLNTLDG 120
 Db 94 CWAQDPLPDPASEGDEQVKELRAREKIPDDYFVVLGDMITEALPTYCTMLNTLDG 153

QY 121 VRDETGAAPTWSAINTRWTAEENRHGDLLNKYLISGRVDRQIETKTQYLIGSGMDPR 180
 Db 154 VRDETGAAPTWSAINTRWTAEENRHGDLLNKYLISGRVDRQIETKTQYLIGSGMDPR 213

QY 181 TENSPLYGLFIYTSPQERATFISHGNTARQAKHDKLAQIGTIAADEKRHETATKIV 240
 Db 214 TENSPLYGLFIYTSPQERATFISHGNTARQAKHDKLAQIGTIAADEKRHETATKIV 273

QY 241 EKLFELIDPDGTVLAFADMRRKIKISMPAHLYMDGRDDNLFDHFSAVAORLGVTAKDYADI 300
 Db 274 EKLFELIDPDGTVLAFADMRRKIKISMPAHLYMDGRDDNLFEHFSAVAORLGVTAKDYADI 333

QY 301 LEFLVGRWKVDKTKTGLSAEGQRQDYYCRLPPRIRRLBERAGRAKADAPTMSFWSDRQ 360
 Db 334 LEFLVGRWKVADLTGLSGEGRKAQDYYCGLPPRIRRLBERAGRAKEGPVVDFSWIDRQ 393

QY 361 VKL 363
 Db 394 VKL 396

RESULT 10
 PCT-US91-01746-13
 Sequence 13, Application PC/TUS9101746
 GENERAL INFORMATION:
 APPLICANT: Thompson, Gregory A.
 APPLICANT: Knauf, Vic C
 TITLE OF INVENTION: Plant Desaturases-Compositions and Uses
 NUMBER OF SEQUENCES: 43
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Calgene, Inc.
 STREET: 1920 Fifth Street
 CITY: Davis
 STATE: California
 COUNTRY: USA
 ZIP: 95616

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB storage
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Macintosh 6.0.7
 SOFTWARE: MicrosoftWord 4.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US91/01746
 FILING DATE: 19910314
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 07/615,784
 FILING DATE: 14-NOV-1990
 APPLICATION NUMBER: 07/567,373
 FILING DATE: 13-AUG-1990
 APPLICATION NUMBER: 07/494,106

FILING DATE: 16-MAR-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Lassen, Elizabeth
 REGISTRATION NUMBER: 31,845
 NAME: Donna E. Scherer
 REGISTRATION NUMBER: 34,719
 REFERENCE/DOCKET NUMBER: CGNE 69-3 WO
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (916) 753-6313
 TELEX: 350370 CGNE
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 396 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US91-01746-13

Query Match 91.4%; Score 1752; DB 5; Length 396;
 Best Local Similarity 90.1%; Pred. No. 3e-164; Indels 0; Gaps 0;

Matches 327; Conservative 18; Mismatches 18; Indels 0; Gaps 0;

Qy 1 ASTLKGSKVEYNLKKPFMPPREHYQVTHSMPPKTEIFKSLDNWAENILVHLKPKVEK 60
 Db 34 ASTLGSSPKVDNAKKPFPQBPREVHQVTHSMPPKTEIFPKSIEWAEQNILVHLKPKVEK 93

Qy 61 CWQOPDFLPDASDGDEQVRELREPAKEFDDYFWVLGDMITEALPYYQTMLNTLDG 120
 Db 94 CWOAQOPFLPDASEGKELRARAKEFDDYFWVLGDMITEALPYYQTMLNTLDG 153

Qy 121 VRDETGAStPSIAWTRAWTAEENRGDLANKLYLSGRDMDQEKTIQYLIGSGMDPR 180
 Db 154 VRDETGAStLTPWAVNTRAWTAEENRGDLANKLYLSGRDMDRQIQTQYLIGSGMDPR 213

Qy 181 TENSPIGFITSQERATFISHGNTARQAEHGDIKLQAQICGTIAADEKRHETAYTKIV 240
 Db 214 TENSPIGFITSQERATFISHGNTARHAKDHGDVKLAQICGTIASDEKRHETAYTKIV 273

Qy 241 EKLFDIPDGTVLAFADMRRKTSMPAHLYGDRDNLFESAYAQRQLGYTAYDADI 300
 Db 274 EKLFDIPDGTVLAFADMRRKTSMPAHLYGDRDNLFESAYAQRQLGYTAYDADI 333

Qy 301 LEFLYGRWKVDKLTGSAEGQKAQDYVCRLPPIRIRLEERHQGRAKEAPIMPESWIFDRO 360
 Db 334 LEFLYGRWKVDKLTGSAEGQKAQDYVCRLPPIRIRLEERHQGRAKEAPIMPESWIFDRO 393

Qy 361 VKL 363
 Db 394 VKL 396

RESULT 11
 US-08-471-791-20
 ; Sequence No. 20, Application US/08471791
 ; Patent No. 5723595
 ; GENERAL INFORMATION:
 ; APPLICANT: Thompson, Gregory A.
 ; TITLE OF INVENTION: Plant Desaturases-Compositions
 ; TITLE OF INVENTION: and Uses
 ; NUMBER OF SEQUENCES: 45
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Calgene, Inc.
 ; STREET: 1920 Fifth Street
 ; CITY: Davis
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 95616
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB storage
 ; COMPUTER: Apple Macintosh
 ; OPERATING SYSTEM: Macintosh 7.1

; SOFTWARE: MicrosoftWord 5.1 (a)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/471,791
 ; FILING DATE: 6-JUNE-95
 ; CLASSIFICATION: 435
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 07/762,762
 ; FILING DATE: 16-SEPT-1991
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US91/01746
 ; FILING DATE: 14-MAR-1991
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 07/567,373
 ; FILING DATE: 13-AUG-1990
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 07/615,784
 ; FILING DATE: 07-NOV-1990
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 07/494,106
 ; FILING DATE: 16-MAR-1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lassen, Elizabeth
 ; REGISTRATION NUMBER: 31,845
 ; NAME: Donna E. Scherer
 ; REGISTRATION NUMBER: 31,845
 ; NAME: Carl J. Schwedler
 ; REGISTRATION NUMBER: 36,924
 ; REFERENCE/DOCKET NUMBER: CGNE 69-5
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (916) 753-6313
 ; TELEFAX: (916) 753-1510
 ; TELEX: 350370 CGNE
 ; INFORMATION FOR SEQ ID NO: 20:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 398 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-471-791-20

Query Match 88.6%; Score 1698; DB 1; Length 398;
 Best Local Similarity 88.28%; Pred. No. 6.3e-159; Mismatches 27; Indels 0; Gaps 0;

Matches 314; Conservative 27; Indels 0; Gaps 0;

Qy 8 SKEVENLKKPFMPPREHYQVOTHSMPPKTEIFKSLDNWAENILVHLKPKVEKCMQPDF 67
 Db 43 SKEVESLKKPFMPPKVEHVOLVLSHSMPPKTEIFKSMEDWAECNLITOLKDVKEKSQWPQDF 102

Qy 68 LPDPASDGFDEQVRELREPAKEIPDDYFWVLGDMITEALPYYQTMLNTLDGVREDTGA 127
 Db 103 LPDPASDGFDEQVRELREPALELPDYFWVLGDMITEALPYYQTMLNTLDGVREDTGA 162

Qy 128 SPTSWAIWTRATAEENRGDLANKLYLSGRDMDROEKTIQYLIGSGMDPRTENSPYL 187
 Db 163 SPTSWAIWTRATAEENRGDLANKLYLSGRDMDROEKTIQYLIGSGMDPRTENSPYL 222

Qy 188 GFIYTSFOERATFISHGNTARQAEHGDIKLQAQICGTIAADEKRHETAYTKIVEKLEID 247
 Db 223 GFIYTSFOERATFISHGNTARQAEHGDIKLQAQICGTIAADEKRHETAYTKIVEKLEID 282

Qy 248 PDGTVALADMRKKTSMPAHLYGDRDNLFDHFSAYAQRQLGYTAKDYADLFLYGR 307
 Db 283 PDGTVALADMRKKTSMPAHLYGDRDNLFDHFSAYAQRQLGYTAKDYADLFLYGR 342

Qy 308 WKVDKLUGLSAGQOKAQDYCRLPPIRIRLEERHQGRAKEAPIMPESWIFDROVKL 363
 Db 343 WKESTLPLGSBNSKAQFLCGTTPRRLDEAQAKKGPKVPSWTHDEVQL 398

RESULT 12
 US-08-471-791-20

Sequence 6, Application US/08926522
 Patent No. 6426347
 GENERAL INFORMATION:
 APPLICANT: Vic C. Knauf
 APPLICANT: Gregory A. Thompson
 TITLE OF INVENTION: PLANT SEED OILS
 NUMBER OF SEQUENCES: 23
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Calgene, Inc.
 STREET: 1920 Fifth Street
 CITY: Davis
 STATE: CA
 COUNTRY: USA
 ZIP: 95616
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Macintosh 7.1
 SOFTWARE: Microsoft Word 5.1(a)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/926,522
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/458,173
 FILING DATE: 2-June-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Elizabeth Lassen
 REGISTRATION NUMBER: 31,845
 NAME: Donna E. Scheer
 REGISTRATION NUMBER: 34,719
 NAME: Carl J. Schwedler
 REGISTRATION NUMBER: 36,924
 REFERENCE/DOCKET NUMBER: CGNE DES
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (916) 753-6313
 TELEFAX: (916) 753-1510
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 398 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-926-522-6

Query Match 88.6%; Score 1698; DB 4; Length 398;
 Best Local Similarity 88.2%; Pred. No. 6, 3e-159;
 Matches 314; Conservative 27; Mismatches 15; Indels 0; Gaps 0;

Query 8 SKEVENLKPKMPREHVQVTHSMPPQKIEFKSLDNWAENILVHLKPVEKWCWQDF 67
 Db 43 SKEVESLKPKPFPKEVHQVHSMPQKIEFKSMEDWAENNLQLQDKVSQDF 102

Query 68 LPDPASDFGDFQRELREKAKLPDDYFVVLGDMITEEALPTYQTMINTLGVRDETGA 127
 Db 103 LPDPASDFGDFQRELREKAKLPDDYFVVLGDMITEEALPTYQTMINTLGVRDETGA 162

Query 128 SPTSWA1WTRWAAENRHGDLINKYLSSGVDMDRQKTEKTQYLIGSGMDRTENSPYL 187
 Db 163 SPTSWA1WTRWAAENRHGDLINKYLSSGVDMDRQKTEKTQYLIGSGMDRTENSPYL 222

Query 188 GFYTTSQEGRATFISHGNTARQAKEHGDIKLQAICGTTAADEKRHETAYTKIVEKLFIED 247
 Db 223 GFYTTSQEGRATFISHGNTARQAKEHGDIKLQAICGTTAADEKRHETAYTKIVEKLFIED 282

Query 248 PGTVLAFADMMRKKSMPAHLYMDGRDNLFDHFSAVAORLGVTAKDYADILEFLVGR 307
 Db 283 PGTVMAFADMMRKKSMPAHLYMDGRDNLFDHFSAVAORLGVTAKDYADILEFLVGR 342

Query 308 WKVDKLGSAEQCAQDYVCPLPRRLEQRAGRAKEAFTMPSWIFDQVKL 363
 Db 343 WKTESLGLSGEGNKAQEYLCCGTPRTRLDRAQARAKKGSKVPSWIHOREVQL 398

Query 344 SPPTSWA1WTRWAAENRHGDLINKYLSSGVDMDRQKTEKTQYLIGSGMDRTENSPYL 187
 Db 383 SPPTSWA1WTRWAAENRHGDLINKYLSSGVDMDRQKTEKTQYLIGSGMDRTENSPYL 222

Query 384 GFYTTSQEGRATFISHGNTARQAKEHGDIKLQAICGTTAADEKRHETAYTKIVEKLFIED 247
 Db 423 GFYTTSQEGRATFISHGNTARQAKEHGDIKLQAICGTTAADEKRHETAYTKIVEKLFIED 282

Query 424 PDGTVMAFADMMRKKSMPAHLYMDGRDNLFDHFSAVAORLGVTAKDYADILEFLVGR 307
 Db 463 PDGTVMAPFADMMRKKSMPAHLYMDGRDNLFDHFSAVAORLGVTAKDYADILEFLVGR 342

Qy 308 WVKDKLTGLSAEGQKAQDYYCRLPPRIRLEERAOGRAKAPTMPSWIFDRQYKL 363
 Db 343 WKIESLTGSGEGNKAQEYLCGLTPRIRLDERAQARAKGPKVFFSWIHDREVQL 398

RESULT 14
 US-08-539-798-4
 ; Sequence 4, Application US/08539798
 ; Patent No. 5614400
 ; GENERAL INFORMATION:
 ; APPLICANT: CAHOON, Edgar B.
 ; APPLICANT: OHROGEE, John B.
 ; TITLE OF INVENTION: Methods and Compositions Relating to
 ; TITLE OF INVENTION: Plant 6-Delta Palmitoyl-Acy Carrier Protein Desaturase
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pioneer Hi-Bred International, Inc.
 ; STREET: 700 Capital Square, 400 Locust Street
 ; CITY: Des Moines
 ; STATE: Iowa
 ; COUNTRY: US
 ; ZIP: 50309
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: FLOPPY disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; APPLICATION NUMBER: US/08/539,798
 ; FILING DATE:
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/329,560
 ; FILING DATE: 26-OCT-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Yates, Michael E.
 ; REGISTRATION NUMBER: 02844US
 ; REFERENCE/DOCKET NUMBER:
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (515) 248-4800
 ; TELEFAX: (515) 248-4844
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 385 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; US-08-539-798-4

Query Match 68.7%; Score 1316; DB 1; Length 385;
 Best Local Similarity 67.1%; Pred. No. 2.5e-121;
 Matches 247; Conservative 46; Mismatches 55; Indels 20; Gaps 4;

Qy 13 NLKKPFPMPREVHQ -----VTHSMP-----
 Db 17 NMFTRIAPPQAGRVRSKVSMASLHASPYLEDKLAKGRPEDELNLSLEWARDNLVLH 76

Qy 56 KPVKEKWCQPODFLPDPASGDFDEVRLERAKEIPDDYFVVLGDMITEALPTYQTML 115
 Db 77 KSVENSWQPOQYLPDPDSAFQEMRERAKDIPDEYVVLGDMITEALPTYMSML 136

Qy 116 NTLDGVURDETASGPTSWAIWTRAWTAEEHRGDLINKYLVLSGRDQMRQFETKIQYLIGS 175
 Db 137 NRCDG1KDDTGAQPTSWATWTRAWTAEEHRGDLINKYLVLSGRDQMRQFETKIQYLIGS 196

Qy 176 GMDPRTEPSYPLGFITYTSQERATEFISHGNTAARQAEKHGDIKLAQCGTIAADEKRHETA 235
 Db 197 GMDTKTENCPYMGFIITSQERATEFISHANTAKLAQHGDKNLAQCGNADSKERHATA 256

Qy 236 YTKIVEKLFIEDPDGTYLAFADMRRKKISMPAHMLYDGRDDNLFDHFSAYAQRLGVYTA 295
 Db 257 YTKIVEKLAETDPDTVIASFDMRMKIQMPAHAMYDGSDDMLFKHTAVSQSQCIVYSAW 316

Qy 296 DYADILEFLYGRWKVDKLGLSAEGQKAQDYYCRLPPRIRLEERAOGRAKAPTMPSWIFDRQYKL 353
 Db 317 DYCDDILFLVIDWNVAKMTGLSSEGGRKAQETVCSLAAKIRVEEKVQGKERKA-VLDPVAF 375

RESULT 15
 US-08-329-560-4
 ; Sequence 4, Application US/08329560
 ; Patent No. 5614402
 ; GENERAL INFORMATION:
 ; APPLICANT: CAHOON, Edgar B.
 ; APPLICANT: OHROGEE, John B.
 ; TITLE OF INVENTION: Methods and Compositions Relating to
 ; TITLE OF INVENTION: Plant 6-Delta Palmitoyl-Acy Carrier Protein Desaturase
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pioneer Hi-Bred International, Inc.
 ; STREET: 700 Capital Square, 400 Locust Street
 ; CITY: Des Moines
 ; STATE: Iowa
 ; COUNTRY: US
 ; ZIP: 50309
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/329,560
 ; FILING DATE: 26-OCT-1994
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Yates, Michael E.
 ; REGISTRATION NUMBER: 36,063
 ; REFERENCE/DOCKET NUMBER: 02844US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (515) 248-4800
 ; TELEFAX: (515) 248-4844
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 385 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; US-08-329-560-4

Query Match 68.7%; Score 1316; DB 1; Length 385;
 Best Local Similarity 67.1%; Pred. No. 2.5e-121;
 Matches 247; Conservative 46; Mismatches 55; Indels 20; Gaps 4;

Qy 13 NLKKPFPMPREVHQ -----VTHSMP-----
 Db 17 NMFTRIAPPQAGRVRSKVSMASLHASPYLEDKLAKGRPEDELNLSLEWARDNLVLH 76

Qy 56 KPVKEKWCQPODFLPDPASGDFDEVRLERAKEIPDDYFVVLGDMITEALPTYQTML 115
 Db 77 KSVENSWQPOQYLPDPDSAFQEMRERAKDIPDEYVVLGDMITEALPTYMSML 136

Qy 116 NTLDGVURDETASGPTSWAIWTRAWTAEEHRGDLINKYLVLSGRDQMRQFETKIQYLIGS 175
 Db 137 NRCDG1KDDTGAQPTSWATWTRAWTAEEHRGDLINKYLVLSGRDQMRQFETKIQYLIGS 196

Qy 176 GMDPRTEPSYPLGFITYTSQERATEFISHGNTAARQAEKHGDIKLAQCGTIAADEKRHETA 235
 Db 197 GMDTKTENCPYMGFIITSQERATEFISHANTAKLAQHGDKNLAQCGNADSKERHATA 256

Qy 236 YTKIVEKLFIEDPDGTYLAFADMRRKKISMPAHMLYDGRDDNLFDHFSAYAQRLGVYTA 295
 Db 257 YTKIVEKLAETDPDTVIASFDMRMKIQMPAHAMYDGSDDMLFKHTAVSQSQCIVYSAW 316

Qy 296 DYADILEFLYGRWKVDKLGLSAEGQKAQDYYCRLPPRIRLEERAOGRAKAPTMPSWIFDRQYKL 353
 Db 317 DYCDDILFLVIDWNVAKMTGLSSEGGRKAQETVCSLAAKIRVEEKVQGKERKA-VLDPVAF 375

Db 257 YTKEVKLAEIDDDTTVIAFSDDMRKKTQMPAHAMYDGSDDMLFKHFTAVSQIGYSAW 316
Qy 296 DADILLEFLUGRMKVDKLTLGSAEGOKAQDYCRLPPRIRLLEERAQGRAKEAFTIMP--F 353
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 317 DCDBLDEFLVIDKWNVAKMTGLSGEGRRAQEYVCSLAAKIRVEEKVGKERKA-VLPVAF 375
Qy 354 SWIFDROV 361
| | : | : | : |
Db 376 SWIFNRQI 383

Search completed: March 7, 2003, 03:11:02
Job time : 20 secs

Qy	301	LEFLYGRWKVDKLTGLSAEGOKAQDYVCRLPPIRRLLEERAOQGRAKEAAPPMPFSWIFDQ	360	Db	94	CWQPODFLPDPASDGFDQEVRRELREAKEIPDDYFVVLVGDMITEALPTYQTMLNTLDG	153		
Db	334	LEFLYGRWKVDKLTGLSAEGOKAQDYVCRLPPIRRLLEERAOQGRAKEAAPPMPFSWIFDQ	393	Oy	121	VRDETAGSPTSWAIWTRAWTAENRIGDNLNKYLQLSGRVDMRQIEKTJOYLIGSGMDPR	180		
Qy	361	VKL 363		Db	154	VGDETAGSPTSWAIWTRAWTAENRIGDNLNKYLQLSGRVDMRQIEKTJOYLIGSGMDPR	213		
Db	394	VKL 396		Qy	181	TENSPVLFITYTSFQERATEISHGNAQARQAEKHGDKLAQICGTIAADEKREHETATKIV	240		
RESULT 3									
AAR1189	ID	AAR1189 standard; Protein; 396 AA.		Db	214	TENSPVLFITYTSFQERATEISHGNAQARQAEKHGDKLAQICGTIAADEKREHETATKIV	273		
XX	AC	AAR1189;		Qy	241	EKLFEDPDGTVLAFADMMRKKSIMPAAHLYMGRDNLNFDHESAVAOQLGVYTAKDYADI	300		
AC	XX	11-DEC-1991 (first entry)		Db	274	EKLFEDPDGTVLAFADMMRKKSIMPAAHLYMGRDNLNFDHESAVAOQLGVYTAKDYADI	333		
DE	R.	communis delta9 desaturase from pCGN3230.		Qy	301	LEFLYGRWKVDKLTGLSAEGOKAQDYVCRLPPRIRLLEERAGGRKEAAPTMPFSWIFDQ	360		
DE	XX	Desaturase; fatty acid; saturation; chill tolerance; lipid herbicide.		Db	334	LEFLYGRWKVDKLTGLSAEGOKAQDYVCRLPPRIRLQERAGGRKEAAPTMPFSWIFDQ	393		
KW	KW			Qy	361	VKL 363			
XX	OS	Ricinus communis.		Db	394	VKL 396			
XX	PN	WO9113972-A.		RESULT 4					
XX	XX			ID	AAR20011	standard; Protein; 391 AA.			
PD	19-SEP-1991.			XX	AAR20011;				
XX	PF	14-MAR-1991;	91WO-U001746.	AC	AC				
XX	XX			XX	XX				
PR	14-NOV-1990;	90US-0615784.		DT	DT				
PR	16-MAR-1990;	90US-094106.		XX	XX				
PR	13-AUG-1990;	90US-0567373.		DE	DE				
XX	PA	(CALG-) CALGENE INC.		XX	XX				
XX	PA	Thompson G, Knauf V;		KW	soya bean; plant oil; stearic acid.				
XX	PI	WPI; 1991-295627/40.		XX	XX				
XX	DR	N-PSDB; AAQ13964.		OS	Glycine max strain Cultivar Wye.				
XX	PT	DNA encoding a plant desaturase - used for modifying the satd.		XX	XX				
XX	PT	fatty acid compsn. of plant cells and plant seeds		FH	Key	Location/Qualifiers			
XX	PS	Disclosure: Fig 3B; 128pp; English.		FT	Peptide	1..32			
XX	XX			FT	Peptide	/label= transit			
CC	CC	Modification of fatty acid in a plant host cell to a different		XX	XX	33...391			
CC	CC	percentage of fatty acid satn. is possible by growing a host plant		PD	PD				
CC	CC	cell having integrated into its genome a recombinant DNA sequence		12-DEC-1991.	12-DEC-1991.				
CC	CC	encoding this protein, under the control of regulatory elements		XX	XX				
CC	CC	functional in the plant cell during lipid accumulation, under		16-MAY-1991;	16-MAY-1991;				
CC	CC	conditions which will promote the activity of the regulatory elements.		XX	XX	91WO-US03288.			
CC	CC	By increasing the amt. of desaturase available in plant cells, an		25-MAY-1990;	25-MAY-1990;	90US-0529049.			
CC	CC	increased percentage of unsatd. fatty acids may be provided, using		XX	XX				
CC	CC	anti-sense technology, the amt. of desaturase can be decreased,		PA	PA	(DUPO) DU PONT DE NEMOURS CO.			
CC	CC	resulting in a higher percentage of fatty acids.		XX	XX				
CC	CC	Using the desaturase gene and derivs. in cells and plants,		PI	PI	Hitz WD, Yadav N;			
CC	CC	desirable traits such as chill tolerance may be introduced and		XX	XX	WPI; 1992-007469/01.			
CC	CC	environmentally safe herbicide prods. may be provided.		DR	DR	DR N-PSDB; AAQ20187.			
CC	CC	See also AAQ13963-69.		XX	XX				
XX	SQ	Sequence 396 AA;		PS	PS	DNA encoding soybean stearoyl-ACP desaturase enzyme and precursor			
XX	XX			XX	XX	- and chimeric genes, for plant transformation and control of			
CC	CC			PT	PT	levels of satd. and unsaturated fatty acids in edible oils			
CC	CC			XX	XX	Disclosure; Page 54; 70pp; English.			
CC	CC			XX	XX	Query Match 99.3%; Score 1903; DB 12; Length 396;			
CC	CC			CC	CC	Best Local Similarity 99.2%; Pred. No. 2, 3e-170; Mismatches 2; Indels 0; Gaps 0;			
CC	CC			CC	CC	Matches 360; Conservative 2; Scores 1903; DB 12; Length 396;			
CC	CC			CC	CC	See also AAQ20188-Q20190 and AAR20012.			
CC	CC			XX	XX	SQ Sequence 391 AA;			
CC	CC			CC	CC	Query Match 91.5%; Score 1753; DB 13; Pred. No. 2, 9e-156;			
CC	CC			CC	CC	Best Local Similarity 89.8%; Length 391;			
CC	CC			CC	CC	See also AAQ20188-Q20190 and AAR20012.			

PD	19-SEP-1991.	XX	AC	AAR22048;
XX	14-MAR-1991;	91WO-U001746.	XX	
XX	14-NOV-1990;	90US-0615784.	DT	07-JUL-1992 (first entry)
PR	16-MAR-1990;	90US-0494106.	XX	Carthamus tinctorius desaturase.
PR	13-AUG-1990;	90US-0567373.	DE	
XX	(CALG -) CALGENE INC.	KW	Safflower; fatty acid synthesis; seed; acyl carrier protein; lipids.	
XX	Thompson G,	Knauf V;	XX	Carthamus tinctorius.
XX	DR; WPI; 1991-295627/40.	OS	OS	
XX	N-PSDB; AAQ13963.	XX	XX	W09203564-A.
XX	DNA encoding a plant desaturase - used for modifying the satd. fatty acid compsn. of plant cells and plant seeds	PT	PT	05-MAR-1992.
XX	Disclosure: Fig 2; 128pp; English.	PT	PT	15-AUG-1991; 91WO-U005801.
PS	Modification of fatty acid in a plant host cell to a different percentage of fatty acid satn. is possible by growing a host plant cell having integrated into its genome a recombinant DNA sequence encoding this protein, under the control of regulatory elements functional in the plant cell during lipid accumulation, under conditions which will promote the activity of the regulatory elements. By increasing the amt. of desaturase available in plant cells, an increased percentage of unsatd. fatty acids may be provided, using anti-sense technology, the amt. of desaturase can be decreased, resulting in a higher percentage of fatty acids.	CC	CC	26-JUN-1991; 91US-0721761.
CC	Using the desaturase gene and derirs. in cells and plants, environmental traits such as chll tolerance may be introduced and see also AAQ13963-69.	CC	CC	15-AUG-1990; 90US-0568493.
XX	Sequence 396 AA;	SQ	PA	(CALG -) CALGENE INC.
Query Match	91.4%; Score 1752; DB 12; Length 396;	XX	PA	Knauf VC, Thompson GA;
Best Local Similarity	90.1%; Pred. No. 3.7e-156;	XX	XX	XX
Matches	327; Conservative 18; Mismatches 18; Indels 0; Gaps 0;	XX	XX	WPI; 1992-096907/12.
Qy	1 ASTLKGSKVEENLKRKPMPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 60	Db	DR	DR N-PSDB; AAQ222616.
Db	34 ASTLGSSTSPKVDNAKKPFQPPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 93	SQ	XX	XX
Query Match	91.4%; Score 1752; DB 12; Length 396;	XX	XX	New plant beta-ketoacyl synthase protein - obtnd. from Ricinus communis, useful e.g. for modifying fatty acid compsn.
Best Local Similarity	90.1%; Pred. No. 3.7e-156;	XX	XX	XX
Matches	327; Conservative 18; Mismatches 18; Indels 0; Gaps 0;	XX	XX	Disclosure: Fig 8; 157pp; English.
Qy	1 ASTLKGSKVEENLKRKPMPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 60	Db	PS	XX
Db	34 ASTLGSSTSPKVDNAKKPFQPPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 93	SQ	PS	XX
Query Match	91.4%; Score 1752; DB 13; Length 396;	XX	PS	PS
Best Local Similarity	90.1%; Pred. No. 3.7e-156;	XX	XX	XX
Matches	327; Conservative 18; Mismatches 18; Indels 0; Gaps 0;	XX	XX	XX
Qy	1 ASTLKGSKVEENLKRKPMPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 60	Db	DR	DR N-PSDB; AAQ222616.
Db	34 ASTLGSSTSPKVDNAKKPFQPPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 93	SQ	XX	XX
Query Match	91.4%; Score 1752; DB 12; Length 396;	XX	XX	The protein sequence was deduced from the desaturase gene isolated from Carthamus tinctorius as the clone WCN2754. The clone can be used to construct acyl carrier protein expression cassettes in a binary vector for plant transformation. This allows integration of nucleic acids encoding a desaturase sequence and a synthase sequence into the genome of a host cell. A plant desaturase includes any enzyme capable of catalysing the insertion of a first double bond into a fatty acid-ACP moiety especially between C9-C10. See also AAQ13963-53.
Best Local Similarity	90.1%; Pred. No. 3.7e-156;	XX	XX	XX
Matches	327; Conservative 18; Mismatches 18; Indels 0; Gaps 0;	XX	XX	XX
Qy	1 ASTLKGSKVEENLKRKPMPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 60	Db	DR	DR N-PSDB; AAQ222616.
Db	34 ASTLGSSTSPKVDNAKKPFQPPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 93	SQ	XX	XX
Query Match	91.4%; Score 1752; DB 13; Length 396;	XX	XX	XX
Best Local Similarity	90.1%; Pred. No. 3.7e-156;	XX	XX	XX
Matches	327; Conservative 18; Mismatches 18; Indels 0; Gaps 0;	XX	XX	XX
Qy	1 ASTLKGSKVEENLKRKPMPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 60	Db	DR	DR N-PSDB; AAQ222616.
Db	34 ASTLGSSTSPKVDNAKKPFQPPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 93	SQ	XX	XX
Query Match	91.4%; Score 1752; DB 13; Length 396;	XX	XX	XX
Best Local Similarity	90.1%; Pred. No. 3.7e-156;	XX	XX	XX
Matches	327; Conservative 18; Mismatches 18; Indels 0; Gaps 0;	XX	XX	XX
Qy	1 ASTLKGSKVEENLKRKPMPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 60	Db	DR	DR N-PSDB; AAQ222616.
Db	34 ASTLGSSTSPKVDNAKKPFQPPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 93	SQ	XX	XX
Query Match	91.4%; Score 1752; DB 13; Length 396;	XX	XX	XX
Best Local Similarity	90.1%; Pred. No. 3.7e-156;	XX	XX	XX
Matches	327; Conservative 18; Mismatches 18; Indels 0; Gaps 0;	XX	XX	XX
Qy	1 ASTLKGSKVEENLKRKPMPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 60	Db	DR	DR N-PSDB; AAQ222616.
Db	34 ASTLGSSTSPKVDNAKKPFQPPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 93	SQ	XX	XX
Query Match	91.4%; Score 1752; DB 13; Length 396;	XX	XX	XX
Best Local Similarity	90.1%; Pred. No. 3.7e-156;	XX	XX	XX
Matches	327; Conservative 18; Mismatches 18; Indels 0; Gaps 0;	XX	XX	XX
Qy	1 ASTLKGSKVEENLKRKPMPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 60	Db	DR	DR N-PSDB; AAQ222616.
Db	34 ASTLGSSTSPKVDNAKKPFQPPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 93	SQ	XX	XX
Query Match	91.4%; Score 1752; DB 13; Length 396;	XX	XX	XX
Best Local Similarity	90.1%; Pred. No. 3.7e-156;	XX	XX	XX
Matches	327; Conservative 18; Mismatches 18; Indels 0; Gaps 0;	XX	XX	XX
Qy	1 ASTLKGSKVEENLKRKPMPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 60	Db	DR	DR N-PSDB; AAQ222616.
Db	34 ASTLGSSTSPKVDNAKKPFQPPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 93	SQ	XX	XX
Query Match	91.4%; Score 1752; DB 13; Length 396;	XX	XX	XX
Best Local Similarity	90.1%; Pred. No. 3.7e-156;	XX	XX	XX
Matches	327; Conservative 18; Mismatches 18; Indels 0; Gaps 0;	XX	XX	XX
Qy	1 ASTLKGSKVEENLKRKPMPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 60	Db	DR	DR N-PSDB; AAQ222616.
Db	34 ASTLGSSTSPKVDNAKKPFQPPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 93	SQ	XX	XX
Query Match	91.4%; Score 1752; DB 13; Length 396;	XX	XX	XX
Best Local Similarity	90.1%; Pred. No. 3.7e-156;	XX	XX	XX
Matches	327; Conservative 18; Mismatches 18; Indels 0; Gaps 0;	XX	XX	XX
Qy	1 ASTLKGSKVEENLKRKPMPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 60	Db	DR	DR N-PSDB; AAQ222616.
Db	34 ASTLGSSTSPKVDNAKKPFQPPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 93	SQ	XX	XX
Query Match	91.4%; Score 1752; DB 13; Length 396;	XX	XX	XX
Best Local Similarity	90.1%; Pred. No. 3.7e-156;	XX	XX	XX
Matches	327; Conservative 18; Mismatches 18; Indels 0; Gaps 0;	XX	XX	XX
Qy	1 ASTLKGSKVEENLKRKPMPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 60	Db	DR	DR N-PSDB; AAQ222616.
Db	34 ASTLGSSTSPKVDNAKKPFQPPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 93	SQ	XX	XX
Query Match	91.4%; Score 1752; DB 13; Length 396;	XX	XX	XX
Best Local Similarity	90.1%; Pred. No. 3.7e-156;	XX	XX	XX
Matches	327; Conservative 18; Mismatches 18; Indels 0; Gaps 0;	XX	XX	XX
Qy	1 ASTLKGSKVEENLKRKPMPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 60	Db	DR	DR N-PSDB; AAQ222616.
Db	34 ASTLGSSTSPKVDNAKKPFQPPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 93	SQ	XX	XX
Query Match	91.4%; Score 1752; DB 13; Length 396;	XX	XX	XX
Best Local Similarity	90.1%; Pred. No. 3.7e-156;	XX	XX	XX
Matches	327; Conservative 18; Mismatches 18; Indels 0; Gaps 0;	XX	XX	XX
Qy	1 ASTLKGSKVEENLKRKPMPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 60	Db	DR	DR N-PSDB; AAQ222616.
Db	34 ASTLGSSTSPKVDNAKKPFQPPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 93	SQ	XX	XX
Query Match	91.4%; Score 1752; DB 13; Length 396;	XX	XX	XX
Best Local Similarity	90.1%; Pred. No. 3.7e-156;	XX	XX	XX
Matches	327; Conservative 18; Mismatches 18; Indels 0; Gaps 0;	XX	XX	XX
Qy	1 ASTLKGSKVEENLKRKPMPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 60	Db	DR	DR N-PSDB; AAQ222616.
Db	34 ASTLGSSTSPKVDNAKKPFQPPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 93	SQ	XX	XX
Query Match	91.4%; Score 1752; DB 13; Length 396;	XX	XX	XX
Best Local Similarity	90.1%; Pred. No. 3.7e-156;	XX	XX	XX
Matches	327; Conservative 18; Mismatches 18; Indels 0; Gaps 0;	XX	XX	XX
Qy	1 ASTLKGSKVEENLKRKPMPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 60	Db	DR	DR N-PSDB; AAQ222616.
Db	34 ASTLGSSTSPKVDNAKKPFQPPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 93	SQ	XX	XX
Query Match	91.4%; Score 1752; DB 13; Length 396;	XX	XX	XX
Best Local Similarity	90.1%; Pred. No. 3.7e-156;	XX	XX	XX
Matches	327; Conservative 18; Mismatches 18; Indels 0; Gaps 0;	XX	XX	XX
Qy	1 ASTLKGSKVEENLKRKPMPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 60	Db	DR	DR N-PSDB; AAQ222616.
Db	34 ASTLGSSTSPKVDNAKKPFQPPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 93	SQ	XX	XX
Query Match	91.4%; Score 1752; DB 13; Length 396;	XX	XX	XX
Best Local Similarity	90.1%; Pred. No. 3.7e-156;	XX	XX	XX
Matches	327; Conservative 18; Mismatches 18; Indels 0; Gaps 0;	XX	XX	XX
Qy	1 ASTLKGSKVEENLKRKPMPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 60	Db	DR	DR N-PSDB; AAQ222616.
Db	34 ASTLGSSTSPKVDNAKKPFQPPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 93	SQ	XX	XX
Query Match	91.4%; Score 1752; DB 13; Length 396;	XX	XX	XX
Best Local Similarity	90.1%; Pred. No. 3.7e-156;	XX	XX	XX
Matches	327; Conservative 18; Mismatches 18; Indels 0; Gaps 0;	XX	XX	XX
Qy	1 ASTLKGSKVEENLKRKPMPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 60	Db	DR	DR N-PSDB; AAQ222616.
Db	34 ASTLGSSTSPKVDNAKKPFQPPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 93	SQ	XX	XX
Query Match	91.4%; Score 1752; DB 13; Length 396;	XX	XX	XX
Best Local Similarity	90.1%; Pred. No. 3.7e-156;	XX	XX	XX
Matches	327; Conservative 18; Mismatches 18; Indels 0; Gaps 0;	XX	XX	XX
Qy	1 ASTLKGSKVEENLKRKPMPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 60	Db	DR	DR N-PSDB; AAQ222616.
Db	34 ASTLGSSTSPKVDNAKKPFQPPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 93	SQ	XX	XX
Query Match	91.4%; Score 1752; DB 13; Length 396;	XX	XX	XX
Best Local Similarity	90.1%; Pred. No. 3.7e-156;	XX	XX	XX
Matches	327; Conservative 18; Mismatches 18; Indels 0; Gaps 0;	XX	XX	XX
Qy	1 ASTLKGSKVEENLKRKPMPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 60	Db	DR	DR N-PSDB; AAQ222616.
Db	34 ASTLGSSTSPKVDNAKKPFQPPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 93	SQ	XX	XX
Query Match	91.4%; Score 1752; DB 13; Length 396;	XX	XX	XX
Best Local Similarity	90.1%; Pred. No. 3.7e-156;	XX	XX	XX
Matches	327; Conservative 18; Mismatches 18; Indels 0; Gaps 0;	XX	XX	XX
Qy	1 ASTLKGSKVEENLKRKPMPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 60	Db	DR	DR N-PSDB; AAQ222616.
Db	34 ASTLGSSTSPKVDNAKKPFQPPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 93	SQ	XX	XX
Query Match	91.4%; Score 1752; DB 13; Length 396;	XX	XX	XX
Best Local Similarity	90.1%; Pred. No. 3.7e-156;	XX	XX	XX
Matches	327; Conservative 18; Mismatches 18; Indels 0; Gaps 0;	XX	XX	XX
Qy	1 ASTLKGSKVEENLKRKPMPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 60	Db	DR	DR N-PSDB; AAQ222616.
Db	34 ASTLGSSTSPKVDNAKKPFQPPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 93	SQ	XX	XX
Query Match	91.4%; Score 1752; DB 13; Length 396;	XX	XX	XX
Best Local Similarity	90.1%; Pred. No. 3.7e-156;	XX	XX	XX
Matches	327; Conservative 18; Mismatches 18; Indels 0; Gaps 0;	XX	XX	XX
Qy	1 ASTLKGSKVEENLKRKPMPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 60	Db	DR	DR N-PSDB; AAQ222616.
Db	34 ASTLGSSTSPKVDNAKKPFQPPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 93	SQ	XX	XX
Query Match	91.4%; Score 1752; DB 13; Length 396;	XX	XX	XX
Best Local Similarity	90.1%; Pred. No. 3.7e-156;	XX	XX	XX
Matches	327; Conservative 18; Mismatches 18; Indels 0; Gaps 0;	XX	XX	XX
Qy	1 ASTLKGSKVEENLKRKPMPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 60	Db	DR	DR N-PSDB; AAQ222616.
Db	34 ASTLGSSTSPKVDNAKKPFQPPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 93	SQ	XX	XX
Query Match	91.4%; Score 1752; DB 13; Length 396;	XX	XX	XX
Best Local Similarity	90.1%; Pred. No. 3.7e-156;	XX	XX	XX
Matches	327; Conservative 18; Mismatches 18; Indels 0; Gaps 0;	XX	XX	XX
Qy	1 ASTLKGSKVEENLKRKPMPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 60	Db	DR	DR N-PSDB; AAQ222616.
Db	34 ASTLGSSTSPKVDNAKKPFQPPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 93	SQ	XX	XX
Query Match	91.4%; Score 1752; DB 13; Length 396;	XX	XX	XX
Best Local Similarity	90.1%; Pred. No. 3.7e-156;	XX	XX	XX
Matches	327; Conservative 18; Mismatches 18; Indels 0; Gaps 0;	XX	XX	XX
Qy	1 ASTLKGSKVEENLKRKPMPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 60	Db	DR	DR N-PSDB; AAQ222616.
Db	34 ASTLGSSTSPKVDNAKKPFQPPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 93	SQ	XX	XX
Query Match	91.4%; Score 1752; DB 13; Length 396;	XX	XX	XX
Best Local Similarity	90.1%; Pred. No. 3.7e-156;	XX	XX	XX
Matches	327; Conservative 18; Mismatches 18; Indels 0; Gaps 0;	XX	XX	XX
Qy	1 ASTLKGSKVEENLKRKPMPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 60	Db	DR	DR N-PSDB; AAQ222616.
Db	34 ASTLGSSTSPKVDNAKKPFQPPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 93	SQ	XX	XX
Query Match	91.4%; Score 1752; DB 13; Length 396;	XX	XX	XX
Best Local Similarity	90.1%; Pred. No. 3.7e-156;	XX	XX	XX
Matches	327; Conservative 18; Mismatches 18; Indels 0; Gaps 0;	XX	XX	XX
Qy	1 ASTLKGSKVEENLKRKPMPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 60	Db	DR	DR N-PSDB; AAQ222616.
Db	34 ASTLGSSTSPKVDNAKKPFQPPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 93	SQ	XX	XX
Query Match	91.4%; Score 1752; DB 13; Length 396;	XX	XX	XX
Best Local Similarity	90.1%; Pred. No. 3.7e-156;	XX	XX	XX
Matches	327; Conservative 18; Mismatches 18; Indels 0; Gaps 0;	XX	XX	XX
Qy	1 ASTLKGSKVEENLKRKPMPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 60	Db	DR	DR N-PSDB; AAQ222616.
Db	34 ASTLGSSTSPKVDNAKKPFQPPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 93	SQ	XX	XX
Query Match	91.4%; Score 1752; DB 13; Length 396;	XX	XX	XX
Best Local Similarity	90.1%; Pred. No. 3.7e-156;	XX	XX	XX
Matches	327; Conservative 18; Mismatches 18; Indels 0; Gaps 0;	XX	XX	XX
Qy	1 ASTLKGSKVEENLKRKPMPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 60	Db	DR	DR N-PSDB; AAQ222616.
Db	34 ASTLGSSTSPKVDNAKKPFQPPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 93	SQ	XX	XX
Query Match	91.4%; Score 1752; DB 13; Length 396;	XX	XX	XX
Best Local Similarity	90.1%; Pred. No. 3.7e-156;	XX	XX	XX
Matches	327; Conservative 18; Mismatches 18; Indels 0; Gaps 0;	XX	XX	XX
Qy	1 ASTLKGSKVEENLKRKPMPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 60	Db	DR	DR N-PSDB; AAQ222616.
Db	34 ASTLGSSTSPKVDNAKKPFQPPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 93	SQ	XX	XX
Query Match	91.4%; Score 1752; DB 13; Length 396;	XX	XX	XX
Best Local Similarity	90.1%; Pred. No. 3.7e-156;	XX	XX	XX
Matches	327; Conservative 18; Mismatches 18; Indels 0; Gaps 0;	XX	XX	XX
Qy	1 ASTLKGSKVEENLKRKPMPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 60	Db	DR	DR N-PSDB; AAQ222616.
Db	34 ASTLGSSTSPKVDNAKKPFQPPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 93	SQ	XX	XX
Query Match	91.4%; Score 1752; DB 13; Length 396;	XX	XX	XX
Best Local Similarity	90.1%; Pred. No. 3.7e-156;	XX	XX	XX
Matches	327; Conservative 18; Mismatches 18; Indels 0; Gaps 0;	XX	XX	XX
Qy	1 ASTLKGSKVEENLKRKPMPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 60	Db	DR	DR N-PSDB; AAQ222616.
Db	34 ASTLGSSTSPKVDNAKKPFQPPREHVQVTSMPPQKIEIKPKSLDWAENILVHLKPVKE 93	SQ	XX	XX
Query Match	91.4%; Score 1752; DB 13; Length 396;	XX	XX	XX
Best Local Similarity	90.1%; Pred. No. 3.7e-156;	XX	XX	XX
Matches	327;			

PR	21-JUL-1999;	99US-0145088.	PR	21-OCT-1999;	99US-0160767.
PR	22-JUL-1999;	99US-0145085.	PR	21-OCT-1999;	99US-0160768.
PR	22-JUL-1999;	99US-0145087.	PR	21-OCT-1999;	99US-0160770.
PR	22-JUL-1999;	99US-0145088.	PR	21-OCT-1999;	99US-0160814.
PR	22-JUL-1999;	99US-0145192.	PR	21-OCT-1999;	99US-0160815.
PR	23-JUL-1999;	99US-0145145.	PR	22-OCT-1999;	99US-0160980.
PR	23-JUL-1999;	99US-0145218.	PR	22-OCT-1999;	99US-0160981.
PR	23-JUL-1999;	99US-0145224.	PR	22-OCT-1999;	99US-0160989.
PR	26-JUL-1999;	99US-0145276.	PR	25-OCT-1999;	99US-0161404.
PR	27-JUL-1999;	99US-0145912.	PR	25-OCT-1999;	99US-0161405.
PR	27-JUL-1999;	99US-0145918.	PR	25-OCT-1999;	99US-0161406.
PR	28-JUL-1999;	99US-0145919.	PR	26-OCT-1999;	99US-0161359.
PR	02-AUG-1999;	99US-0145951.	PR	26-OCT-1999;	99US-0161360.
PR	02-AUG-1999;	99US-0146386.	PR	26-OCT-1999;	99US-0161361.
PR	02-AUG-1999;	99US-0146388.	PR	28-OCT-1999;	99US-0161992.
PR	03-AUG-1999;	99US-0147038.	PR	28-OCT-1999;	99US-0161993.
PR	04-AUG-1999;	99US-0147204.	PR	29-OCT-1999;	99US-0162142.
PR	04-AUG-1999;	99US-0147302.			
PR	05-AUG-1999;	99US-0147260.	Query Match	90.4%	Score 1733; DB 21;
PR	05-AUG-1999;	99US-0147303.	Best Local Similarity	89.4%	Length 401;
PR	06-AUG-1999;	99US-0147304.	Matches	322; Conservative	Pred. No. 2..3e-15;
PR	09-AUG-1999;	99US-0147416.		22; Mismatches	Indels 0; Gaps
PR	09-AUG-1999;	99US-0147493.	Qy	4 LKSGSKVEVENLKKPFPMPREHVQVTHSMPPKOKIEFKSLDNWAEENILVLHKPVKEKQW 63	
PR	10-AUG-1999;	99US-0147935.	Db	42 LSSGPKEVESLKKPFPMPREHVQVLSHSMPPKOKIEFKSMENWAEENILHLHKDVKEKWQ 101	
PR	11-AUG-1999;	99US-0148171.			
PR	12-AUG-1999;	99US-0148341.	Qy	64 PDDFLPDASDGDFEQRERAKEPDYDFVVLGDMITEALPY QTMLNTLDGVRD 123	
PR	13-AUG-1999;	99US-0148565.	Db	102 PDDFLPDASDGDFEQRERAREPDYDFVVLGDMITEALPY QTMLNTLDGVRD 161	
PR	13-AUG-1999;	99US-0148684.			
PR	16-AUG-1999;	99US-0149363.	Qy	124 ERGASPTSWAINTRANTAEENRHGDLLINKYLQLSGRVDPROJEKTIOYLIGSGMDPRTEN 183	
PR	17-AUG-1999;	99US-0149415.	Db	162 ETGASPTSWAINTRANTAEENRHGDLLINKYLQLSGRVDPROJEKTIOYLIGSGMDPRTEN 221	
PR	18-AUG-1999;	99US-0149426.			
PR	20-AUG-1999;	99US-0149722.	Qy	184 SPYLGFLYTSFQERATFISHGNTAROKEHGDKLAQICGTAADEKRHETAYTKIVEKL 243	
PR	20-AUG-1999;	99US-0149723.	Db	222 NPYLGFLYTSFQERATFISHGNTAROKEHGDKLAQICGTAADEKRHETAYTKIVEKL 281	
PR	23-AUG-1999;	99US-0149902.			
PR	23-AUG-1999;	99US-0149930.	Qy	244 FEIDPDGVLAFADEMMRKKISMAPHLMDGRDNLFQHSAVQRGLGYTAKDYLEF 303	
PR	25-AUG-1999;	99US-0150566.	Db	282 FEIDPDGVVMAFADEMMRKKISMAPHLMDGRDNLFQHSAVQRGLGYTAKDYLEF 341	
PR	26-AUG-1999;	99US-0150884.			
PR	27-AUG-1999;	99US-0151065.	Qy	304 LYGRWKVDRKLGLSAGEGKAQDYVCRUPLPRIRLEERAQRGRAKEAPMPFSWIFDROVKL 363	
PR	27-AUG-1999;	99US-0151066.	Db	342 LYGRWKVDRKLGLSAGEGKAQDYVCRUPLPRIRLEERAQRGRAKEAPMPFSWIFDROVKL 401	
PR	30-AUG-1999;	99US-0151303.			
PR	31-AUG-1999;	99US-0151438.	RESULT 1.1		
PR	01-SEP-1999;	99US-0151930.	ID ABB92108		
PR	07-SEP-1999;	99US-0152363.	ID ABB92108		
PR	10-SEP-1999;	99US-0153070.	XX AC		
PR	15-SEP-1999;	99US-0154018.	XX DT	31 MAY-2002 (first entry)	
PR	16-SEP-1999;	99US-0154039.	XX DE	Herbically active polypeptide SEQ ID NO 1319.	
PR	20-SEP-1999;	99US-0154779.	XX XX	Herbicidal; plant; agriculture; herbicide.	
PR	22-SEP-1999;	99US-0155139.	XX OS	Arabidopsis thaliana.	
PR	23-SEP-1999;	99US-0155486.	XX PN	WO200210210-A2.	
PR	28-SEP-1999;	99US-0155659.	XX XX	07-FEB-2002.	
PR	29-SEP-1999;	99US-0156458.	XX XX	XX	
PR	12-OCT-1999;	99US-0156596.	XX PR	28-AUG-2001; 2001WO-EPO9892.	
PR	13-OCT-1999;	99US-0157117.	XX PA	(FARB) BAYER AG.	
PR	05-OCT-1999;	99US-0157294.	XX XX	28-AUG-2001; 2001WO-EPO9892.	
PR	13-OCT-1999;	99US-0157753.	XX PR	Tietjen K, Weidler M;	
PR	06-OCT-1999;	99US-0158295.			
PR	07-OCT-1999;	99US-0158765.			
PR	14-OCT-1999;	99US-0159339.			
PR	14-OCT-1999;	99US-0159339.			
PR	14-OCT-1999;	99US-0159637.			
PR	14-OCT-1999;	99US-0159638.			
PR	18-OCT-1999;	99US-0159584.			
PR	21-OCT-1999;	99US-0160741.			

XX WPI; 2002-269010/31.
 XX
 PT Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant organisms -
 PT from plant with nucleic acid or amino acid sequences from non-plant organisms -
 PT
 PS Claim 5; SEQ ID NO 1319; 261PP + Sequence Listing; English.

XX The invention relates to identifying target proteins (ABB0790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as herbicides.

XX Sequence 401 AA;

Query Match 90.4%; Score 1733; DB 23; Length 401;
 Best Local Similarity 89.4%; Pred. No. 2.3e-154;
 Matches 322; Conservative 22; Mismatches 16; Indels 0; Gaps 0;

Oy 4 LKSGSKEVENLKKPMPMPREYHVQVTHSMPPQKIEIFKSLDWNAAEENILVHLKPVEKCHQ 63
 Db 42 LSGGPKVEESLKKPPTPREYHVQVLHSMPQKIEFKSMENAAEENILVHLKDVEKSMQ 101
 Qy 64 PQDFELDPASDGDFEQQRELAKEIPDDYFVVLGDMTEEAALPTYCQMLNTLDGVRD 123
 Db 102 PQDFELDPASDGDFEQQRELAKEIPDDYFVVLGDMTEEAALPTYCQMLNTLDGVRD 161
 Qy 124 ETGASPTSWAINTRATAENRHGDLLNKLYLGSRVDMRQEKTQYLGSMDPRTE 183
 Db 162 ETGASPTSWAINTRATAENRHGDLLNKLYLGSRVDMRQEKTQYLGSMDPRTE 221
 Qy 184 SPYLGFLYTTSQERATFISHGNTAROAKEHCDIKLAQICGTIAADEKRHETAYTKIVEKL 243
 Db 222 NPYLGFYTTSQERATFISHGNTAROAKEHCDIKLAQICGTIAADEKRHETAYTKIVEKL 281
 Qy 244 FEIDPGTVALFADMRRKKISMPAHLYMDGRDNLDHFSAVAORLGYTAKDYADILEF 303
 Db 282 FEIDPGTVALFADMRRKKISMPAHLYMDGRDNLDNFSSVAQRUGVYTAKDYADILEF 341
 Qy 304 LYGRWKVDKLTGLSAEGQKAODYVCRLLPIRRLEBRAQGRAKEAPTMPSWIEDRQVKL 363
 Db 342 LYGRWKVDKLTGLSGEGNKAQDYLCLGAPRKRLDRAQAKKGPKIPSWIHREVQL 401

RESULT 12
 ABB07379
 ID ABB07379 standard; Protein; 401 AA.
 XX
 AC ABB07379;
 XX
 DT 09-APR-2002 (first entry)

XX A. thaliana stearoyl-ACP desaturase (SS12) protein sequence.
 XX
 KW SS12; Arabidopsis; pathogen; plant defence response; enzyme; plant; stearoyl-ACP desaturase; delta9 fatty acid desaturase; stearoyl-ACP; gene therapy.
 XX Arabidopsis thaliana.
 OS
 PN WO20196363-A1.
 XX
 PD 20-DEC-2001.
 XX
 PF 18-MAY-2001; 2001WO-US16134.

PR 12-JUN-2000; 2000US-210967P.
 XX
 PA (BOYC-) BOYCE THOMPSON INST PLANT RES.
 PA (RUTF) UNIV RUTGERS STATE NEW JERSEY.
 PA (UNIV) UNIV KANSAS STATE RES FOUND.
 XX
 PI Klessig DF, Kachroo P, Shah J;
 XX
 WPI: 2002-139703/18.
 DR N-PSDB; ABA4565, ABA4566.
 XX
 PT Novel isolated nucleic acid molecule comprising SS12 gene encoding PT stearoyl-acyl carrier protein desaturase in plants, which when reduced PT or prevented, is useful for enhancing resistance of plant to plant PT pathogens.
 XX
 PS Claim 8; Page 73-74; 80pp; English.
 XX
 CC The invention relates to a novel plant gene, SS12, isolated from CC Arabidopsis thaliana (AT) chromosome 2 at a location within 0.2 cm from CC marker AthB1.02 and 3.7 cm from marker GBF, the disruption of which is CC associated with altered resistance of a plant to plant pathogens or other CC disease causing agents. SS12 encodes a stearoyl-ACP desaturase in plants CC and plays a key role in modulating plant defence responses. The enzyme is CC a delta9 fatty acid desaturase that preferentially desaturates stearoyl- CC ACP (18:0 ACP). Methods using the SS12 gene are provided for enhancing CC the resistance of a plant to plant pathogens or other disease causing CC agents. Transgenic plants lacking SS12 protein, altered fatty acid CC metabolism or enhanced resistance to a selected plant pathogen, can be CC used for plant breeding or directly in agricultural or horticultural CC applications. SS12 DNA, RNA, or their fragments may be used as probes to CC detect the presence and/or expression of SS12 genes. SS12 nucleic acids CC may be utilized as probes in assays such as in situ hybridization; Southern CC hybridization; Northern hybridization and assorted amplification CC reactions such as PCR. Antibodies that are immunologically specific for CC SS12 may be utilized in affinity chromatography to isolate the SS12 CC protein to quantify the SS12 protein, or to immuno-precipitate SS12 from CC a sample containing a mixture of proteins and other biological materials. CC The ss12 mutants display a unique combination of defence responses that CC include constitutive HR and expression of PR genes and enhanced disease CC resistance to certain plant pathogens, and therefore can be used to CC improve crop and horticultural plant species by customizing the defence CC response. The ss12 mutants can be used to identify and isolate additional CC members of this disease resistance pathway. The SS12 transgenic plants CC are useful in conferring the SS12 phenotype to many different plant CC species. A plant with increased functional SS12 has additional defence CC response properties consistent with increased production of the SS12- CC associated fatty acid (FA)-derived signal molecule(s). Similarly, plants CC that have increased production or activity of the SS12 FA desaturase CC display broad resistance to various plant pathogens. The present CC sequence represents the A. thaliana stearoyl-ACP desaturase.
 XX
 SQ Sequence 401 AA;

Query Match 90.4%; Score 1733; DB 23; Length 401;
 Best Local Similarity 89.4%; Pred. No. 2.3e-154;
 Matches 322; Conservative 22; Mismatches 16; Indels 0; Gaps 0;

Oy 4 LKSGSKEVENLKKPMPMPREYHVQVTHSMPPQKIEFKSLDWNAAEENILVHLKPVEKCHQ 63
 Db 42 LS GGPKVEESLKKPPTPREYHVQVLHSMPQKIEFKSMENAAEENILVHLKDVEKSMQ 101
 Qy 64 64 LSSGPKEVESLKKPPTPREYHVQVLHSMPQKIEFKSMENAAEENILVHLKDVEKSMQ 101
 Db 102 PDDFLPDASDGDFEQQRELAKEIPDDYFVVLGDMTEEAALPTYCQMLNTLDGVRD 123
 Qy 124 ETGASPTSWAINTRATAENRHGDLLNKLYLGSRVDMRQEKTQYLGSMDPRTE 183
 Db 162 ETGASPTSWAINTRATAENRHGDLLNKLYLGSRVDMRQEKTQYLGSMDPRTE 221
 Qy 184 SPYLGFLYTTSQERATFISHGNTAROAKEHCDIKLAQICGTIAADEKRHETAYTKIVEKL 243
 Db 222 NPYLGFYTTSQERATFISHGNTAROAKEHCDIKLAQICGTIAADEKRHETAYTKIVEKL 281
 Qy 244 FEIDPGTVALFADMRRKKISMPAHLYMDGRDNLDHFSAVAORLGYTAKDYADILEF 303
 Db 282 FEIDPGTVALFADMRRKKISMPAHLYMDGRDNLDNFSSVAQRUGVYTAKDYADILEF 341
 Qy 304 LYGRWKVDKLTGLSAEGQKAODYVCRLLPIRRLEBRAQGRAKEAPTMPSWIEDRQVKL 363
 Db 342 LYGRWKVDKLTGLSGEGNKAQDYLCLGAPRKRLDRAQAKKGPKIPSWIHREVQL 401

RESULT 12
 ABB07379
 ID ABB07379 standard; Protein; 401 AA.
 XX
 AC ABB07379;
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE A. thaliana stearoyl-ACP desaturase (SS12) protein sequence.
 XX
 KW SS12; Arabidopsis; pathogen; plant defence response; enzyme; plant; stearoyl-ACP desaturase; delta9 fatty acid desaturase; stearoyl-ACP; gene therapy.
 XX Arabidopsis thaliana.
 OS
 PN WO20196363-A1.
 XX
 PD 20-DEC-2001.
 XX
 PF 18-MAY-2001; 2001WO-US16134.

Qy 184 SPYLGFLYTTSQERATFISHGNTAROAKEHCDIKLAQICGTIAADEKRHETAYTKIVEKL 243
 Db 222 NPYLGFYTTSQERATFISHGNTAROAKEHCDIKLAQICGTIAADEKRHETAYTKIVEKL 281

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